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OM protein - protein search, using sw model

Run on: June 23, 2005, 09:47:53 ; Search time 30.4577 Seconds
(without alignments)
882.327 Million cell updates/sec

Title: US-09-830-972-2-FUSED
Perfect score: 1823
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIOAKIPLKRRAD 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	49.6	199	2	US-08-700-607-1
2	904	49.6	201	4	US-09-949-016-9124
3	826.3	45.3	776	2	US-08-700-607-5
4	826.3	45.3	776	4	US-09-949-016-6998
5	816.7	44.8	439	4	US-09-949-016-9180
6	790	43.3	356	2	US-08-700-607-6
7	683	37.5	208	2	US-08-700-607-7
8	669	36.7	267	2	US-08-700-607-8
9	625.9	34.3	192	4	US-09-949-016-8859
10	585.3	32.1	588	4	US-09-949-016-7290
11	548.1	30.1	241	2	US-08-700-607-3
12	539.9	29.6	168	4	US-09-149-476-563
13	522	28.6	219	4	US-09-270-767-45132
14	286.8	15.7	68	4	US-09-513-999C-6304
15	286	15.7	92	4	US-09-149-476-411
16	262.8	14.4	1027	4	US-09-902-540-11750
17	262.5	14.4	75	4	US-09-621-976-4600
18	262.5	14.4	75	4	US-09-621-976-4601
19	253.2	13.9	1255	2	US-09-080-897-4
20	253.2	13.9	1255	3	US-08-899-595-1
21	252.5	13.9	1255	3	US-09-323-735-4
22	252.5	13.9	1248	2	US-09-080-897-2
23	252.5	13.9	1248	3	US-09-323-735-2
24	250	13.7	114	4	US-09-513-999C-7861
25	248.8	13.6	1315	3	US-08-899-595-3
26	241.5	13.2	744	4	US-09-902-540-15347
27	240.6	13.2	990	4	US-09-949-016-10562

28	238.5	13.1	1318	4	US-10-237-551-197	Sequence 197, Appl
29	236.6	13.0	933	3	US-08-764-870-14	Sequence 14, Appl
30	236.6	13.0	933	3	US-08-980-115-14	Sequence 14, Appl
31	236.3	13.0	2142	4	US-09-538-092-1142	Sequence 1142, Ap
32	236.2	13.0	1326	4	US-09-688-188B-15	Sequence 15, Appl
33	236.2	13.0	1326	4	US-09-291-417D-15	Sequence 15, Appl
34	235.7	12.9	8991	4	US-08-714-741-32	Sequence 32, Appl
35	235.1	12.9	1290	4	US-09-248-796A-20654	Sequence 20654, A
36	230.6	12.6	1560	4	US-09-264-512B-2	Sequence 2, Appli
37	230.4	12.6	1341	4	US-09-949-016-6890	Sequence 6890, Ap
38	230.4	12.6	1344	4	US-09-949-016-10925	Sequence 10925, A
39	228.8	12.6	1070	3	US-08-922-635-22	Sequence 22, Appl
40	228.8	12.6	1504	4	US-09-364-206-2	Sequence 2, Appli
41	228.4	12.5	1021	4	US-09-902-540-16773	Sequence 16773, A
42	228	12.5	1089	4	US-09-949-016-9707	Sequence 9707, Ap
43	227.4	12.5	802	4	US-09-823-240A-2	Sequence 2, Appli
44	226.9	12.4	1187	1	US-08-320-559-28	Sequence 28, Appl
45	226.9	12.4	1187	3	US-08-545-860D-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCES/DOCKET NUMBER: PF-0114 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Consensus
; LIBRARY:
US-08-700-607-1

Query Match 49.6%; Score 904; DB 2; Length 199;
Best Local Similarity 97.3%; Pred. No. 1.6e-33;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 173 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232

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Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVIOAI 71
QY 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVL 292
Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVL 131
QY 293 MVVFTYVGFALFNGLTLLIALLSLFSIPVIYERHQQVQIDHYGLANKSVKDMAKIOAKI 352
Db 132 MVVFTYVGFALFNGLTLLIALLSLFSIPVIYERHQQVQIDHYGLANKSVKDMAKIOAKI 191
QY 353 PGLKRRAD 360
Db 192 PGLKRRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 49.6%; Score 904; DB 4; Length 201;
Best Local Similarity 97.3%; Pred. No. 1.6e-33;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 173 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVIOAI 232
Db 14 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIFRIYKGVIOAI 73
QY 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVL 292
Db 74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVL 133
QY 293 MVVFTYVGFALFNGLTLLIALLSLFSIPVIYERHQQVQIDHYGLANKSVKDMAKIOAKI 352
Db 134 MVVFTYVGFALFNGLTLLIALLSLFSIPVIYERHQQVQIDHYGLANKSVKDMAKIOAKI 193
QY 353 PGLKRRAD 360
Db 194 PGLKRRAE 201

RESULT 3
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

Query Match 45.3%; Score 826.3; DB 2; Length 776;
Best Local Similarity 27.7%; Pred. No. 7e-29;
Matches 195; Conservative 52; Mismatches 91; Indels 367; Gaps 17;

QY 10 VSSSTDS-----PPR-----19
Db 85 VSSAMDHFTSTSKDGEVCYTSLSIDICYPPQEDSTYFTGLOKENGHVITISESPEELG 144
QY 20 -PPP-----AFKQFVTEPED 34
Db 145 TPGSLPDVPGIESKGLFSSDGIEMTPAESTEVNKLADPLDQWKAERKIYDITRPEE 204
QY 35 EDEDEEEDDED-----DED-----50
Db 205 VKHQHQHPELEDKDLDFKNKDTDISIKPEGVREPDKAPVBEKIKDHLLESTFAPVI 264
QY 51 -----LEELE-----55
Db 265 DDLSEORRAPQITTPVKITLITEIPSVETTTQKTPKQDICKLPSPDVTPTVTVSEPE 324
QY 56 -----VLERKPAAGLS-----66
Db 325 DDSPGSIPTSPSGTSPSAESQCKGISSEDELIITAIEAKGLSYETAENPRPVQLADRP 384
QY 67 ---AAAVPPAAAPLLDFSDSV-----PPA 89
Db 385 EVKARSGPPTIPSP-LDHEASSAESGDSIEILVSDPMAAEDALPSGVVFGHVGPPPS 443
QY 90 PRGPL-----PAAPPA-----100
Db 444 PASPSIQYILREEREALDSELIIESCDASSASESPKREQDSPMKPSALDAIREETG 503
QY 101 --APERQPS-----WERSPAAPAPSLPPA-----AAVLPKLPEDD-----E 135
Db 504 VRAEERAFSRRCGLAEPGSLFDYPSTEPQGPGLPDGDGALEPETMPLPK-PEESSSNQ 562
QY 136 PPAREPPPPAGASPLABPAAPPSTPAAPKRGSGSSVVDLYWRDIKKTGVVFGASLFL 195
Db 563 SPATKGPGLG-----PGAPPPULFLNKQK-----AIDLLYWRDIKKTGVVFGSFLLL 611
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Db 352 EARRFLVDLSDLSKFAVLMWLLTYVGFALFNGLTLLMAVSMFTLPVYVVKHQAIQDQ 411
QY 333 YLGLANKSVKDAWAKIQAIPGLKRAKAD 360
Db 412 YLGLVRTHINAVVAKIQAIPGAKRHA 439

RESULT 6
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

Query Match 43.3%; Score 790; DB 2; Length 356;
Best Local Similarity 44.1%; Pred. No. 7e-28;
Matches 177; Conservative 47; Mismatches 87; Indels 90; Gaps 15;
QY 2 EDIDQSSLYS--STDSPRRP--PAFYQFVTEPEDEE--DEE-----EEDEE 45
Db 4 EDALPSGYVSFGHVGPPSPSPSIQYSLREAREALDSLIIESCDASSASESPKR 63
QY 46 EDEDELEEVLERKCPAAGLSAAVPPAAAPLLDFSSDV-----PPAPRGL 94
Db 64 EQDS-----PPMKPSAL-----DAIRETGVAERAPSRRG-- 95
QY 95 PAAPAA---PERQSWERSPAAPAPSLPPA-----AAVLPSKLPEDD-----EPPAR 139
Db 96 -LAEPGSLDYSTETEQ-----PGPELPPGDALEPETPMLPRK--PREDSSNQSPAA 146
QY 140 PPPPPAGASPLAEAPSTPAAPKRRGSGSVVLLLYWRDIKKTGVVFGASLFLLSL 199
Db 147 TKGPGPLG-----PGAPPPPLFLNKQK-----AIDLLYWRDIKQTGIVFGSFLLSL 195

QY 200 TVFSIVSVTAYTALALLSVTISFRYKGVIOAKIOKSDGHPFRAYLESEVAISELVOKY 259
Db 196 TQFSVSVSVAYLALAALSATISFRYKSVLQAVQKTDGHPFRAYLELEITUSQEQIKY 255
QY 260 SNSALGHVNSTIKELRRLFLVDLSDLSKFAVLMWVFTYVGFALFNGLTLLILALISLFSI 319
Db 256 TDCLOFYVNSTLKELRRLFLVDLSDLSKFAVLMWLLTYVGFALFNGLTLLILMAVSMFTL 315
QY 320 PVYIERHQVQIDHYLGLANKSVKDAWAKIQAIPGLKRAKAD 360
Db 316 PVYVVKHQAIQDQYLGVRTHINAVVAKIQAIPGAKRHA 356

RESULT 7
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match 37.5%; Score 683; DB 2; Length 208;
Best Local Similarity 67.4%; Pred. No. 1.8e-23;
Matches 128; Conservative 31; Mismatches 31; Indels 0; Gaps 0;
QY 171 SSVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALISVTISFRYKGVQ 230
Db 19 SQAILLYWRDIKQTGIVFGSFLLSLTVFSIVSVVAYLALALASATISFRYKSVLQ 78
QY 231 ATKSDGHPFRAYLESEVAISELVOKYSNSALGHVNSTIKELRRLFLVDLSDLSKFA 290
Db 79 AVQKTDGHPFRAYLELEITLSQEQIKYTDCLQFVNSTLKELRRLFLVDLSDLSKFA 138
QY 291 VLMWVFTYVGFALFNGLTLLILALISLFSIPVYIERHQVQIDHYLGLANKSVKDAWAKIQA 350
Db 139 VLMWLLTYVGFALFNGLTLLILMAVSMFTLPVYVVKHQAIQDQYLGVRTHINAVVAKIQA 198

QY 8 SLVSSDTPPPPPPAFAKQFVTE-PEDEED-----EEEEDEED----- 47
Db 59 STASSTPDS-----TEGNDSDDFRELHAREFSEDEETTSQDWGTPREL 105
QY 48 -----DEDLLEVLERKPAAG 64
Db 106 TSYIAFDGVGSGRRDSTARPRQGRSVSEPRDQHPQPSLGDSLESIPLSQSPERG 165
QY 65 LSAAVPPAAAAPLDFSDSVPAPR-----GPL 94
Db 166 RRG-----DDTAPPSEKPLEDLRLDLHLGWARGTGSGEDSDSTSSSTPL 211
QY 95 PAAPPAAPER-----QPSWERSPAAPAPSL-----PPAAVLPK-- 129
Db 212 EDEEPOEPNRLTGEAGEELDLRLAAPS---SPEVLTPQLSPGSGTPOAGTPSPRSR 268
QY 130 -----LPDEDE---PPARPP-----PPPPAGAS----- 149
Db 269 DNSNGEPEELBEEKQWGLEPFRVGGCLDSTDQLEFTVPRLLGTAMWLKTSLLA 328
QY 150 -----PLAEPAP-----PSTPA-----APKRRG-----SGSSV 173
Db 329 VYKTVFELSPLWTAIGVQGPPTPTFVLRLVLLKWAQSPSSGVPSSLGADMGSKV 388
QY 174 VLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 233
Db 389 ADLLYWKDRTSGVWFTGLMSLCLLHFSIVSVAHLALLCGTISLRVYRKVLQAVH 448
QY 234 KSDGHPFRAYLESEVAISELVOKYSNLSALGHVNSTIKELRLFLVDDVLSLKFVLM 293
Db 449 RGDGANPQAYLDVDTLTREQTERLSHOITSRVSAATQLRHFFLVEDVLSLKALLF 508
QY 294 WYFTVYVGALENGTLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIQA 353
Db 509 YILTFVGAIFNGLTLLILGVLFTPLLYRHOQAQIDQYVGLVTNQLSHIRAKIRAKIP 568
QY 354 GL-----KPKAD 360
Db 569 GTGALASAAAANVSGSKAKAE 588

RESULT 11
US-08-700-607-3
Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: THP1NOB01
CLONE: 31870
US-08-700-607-3
Query Match 30.1%; Score 548.1; DB 2; Length 241;
Best Local Similarity 44.4%; Pred. No. 3e-17;
Matches 111; Conservative 40; Mismatches 60; Indels 39; Gaps 3;
QY 109 EESPAAPAPSLPPAAAVLPKLPDEPPARPPPPPPAGASPLARPPAAPPSTPAAPKRRG 168
Db 3 EXAATQSHSISSSSF-----GAEPSPGGGGSPGACPA-----LGTKSCS 43
QY 169 SGSSVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 228
Db 44 SSCAVHDLIXWEDVKKTGTFVGTLLMLLSLAAFSVISVSYLLALLSVTISFRIYKSV 103
QY 229 IOAIQKSEGHFPFRAYLESEVAISELVOKYSNLSALGHVNSTIKELRLFLVDDVLSLK 288
Db 104 IOAQKSEGHFPFRAYLESEVAISELVOKYSNLSALGHVNSTIKELRLFLVDDVLSLK 163
QY 289 FAVLWMTYVYVGALENGTLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKI 348
Db 164 LAVFWLMTYVYVGALENGTLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKI 203
QY 349 QAKIFGLKREK 358
Db 204 PSKTPWNRQK 213

RESULT 12
US-09-149-476-563
Sequence 563, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
CURRENT APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23


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; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match      29.6%; Score 539.9; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.6e-17;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

QY 195 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISEE 254
DB 1 LLLSLAAFSVISVSYLLIALLSVTISFRIYKSVIOAQVQKSEGHPPKAYLDVDTLSSE 60

QY 255 LVQKYSNSALGHVNSTIKELRLFLVDDLVLSKFAVLMWVTYVYVGLNGLTLLILALI 314
DB 61 AFHYNMAAMVHNRALKLIIRFLVEDLVLSKLAFLVFMWMTYVYVGAVENTLLILABEL 120

QY 315 SLFSPVIVYERHQVQIDHYGLANKSVKDMAKIOPGL-KRXAD 360
DB 121 LIFSVPVIVYKXTQIDHVGVIARDQTSIVEIKIQAQKPGIAKKAE 167

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RESULT 13
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132

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Query Match      28.6%; Score 522; DB 4; Length 219;
Best Local Similarity 50.5%; Pred. No. 3.8e-16;
Matches 95; Conservative 43; Mismatches 50; Indels 0; Gaps 0;

QY 166 RRGSGSVVDLYWRDKTKTVGVFGASLFLLSLVTVFSIVSVTAYIALALLSVTISFRIY 225
DB 16 RQMSNRLLSLIWRDVKKSGIVFGAGLITLAAISSFSVISVFAVLSLTFLFTGVAFRY 75

QY 226 KGVIOAIQKSDGHPFRAYLSEVAISELVOKYSNSALGHVNSTIKELRLFLVDDLYD 285
DB 76 KSTQVAVQNTKEHPKFDLDTLUSHEKVQNIAGVAHNGFISELRLFLVEDIID 135

QY 286 SLKFAVLMWVTYVYVGLNGLTLLILALISLFSIPVYERHQVQIDHYGLANKSVKDMAM 345
DB 136 SIKFGVILWVTYVYVGAWNGMTLVILAFVSLFLPKVYNNKQSIDTHLDLVRSLKTEIT 195

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QY 346 AXIQAKIP 353
DB 196 DKIRVAIP 203

RESULT 14
US-09-513-999C-6304
; Sequence 6304, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6304
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6304

Query Match      15.7%; Score 286.8; DB 4; Length 68;
Best Local Similarity 85.7%; Pred. No. 1.9e-06;
Matches 60; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

QY 1 MEDIDQSLVSSTDSPPRPFPAPFYQVTPEDDEDEDEDEDEDEDEDEDEDEDELEVLK 60
DB 1 MEDLDQSLVSSS-DSPRPQAPFYQVREPEDEE-BEEEEDEDEDEDELEVLK 58

QY 61 PAAGLSAAAV 70
DB 59 PAAGLSAAAV 68

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RESULT 15
US-09-149-476-411
; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597

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[illegible]

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EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 15.7%; Score 286; DB 4; Length 92;
Best Local Similarity 56.0%; Pred. No. 3.6e-06;
Matches 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;
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Db 2 NAAMVHINRALKLIIIRLEFLVEDLVDLSKLAVFNMVMTYVGVFNGITLLILAEELLFSVP 61
Qy 321 VIYERHQVQIDHYHGLANKSVKDAMAKIOAK 351
Db 62 IVEKYKQIDHYVGIARDOTKSIVEKIPSK 92

Search completed: June 23, 2005, 10:17:47
Job time : 32.4577 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 09:56:59 ; Search time 108.849 Seconds
(without alignments)
1271.831 Million cell updates/sec

Title: US-09-830-972-2-FUSED
Perfect score: 1823
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

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Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1817	99.7	360	9 US-09-893-348-20	Sequence 20, Appl
2	1817	99.7	360	16 US-10-810-653-20	Sequence 20, Appl
3	1808.1	99.2	379	14 US-10-205-194-164	Sequence 164, App
4	1732.7	95.0	1163	9 US-09-893-348-18	Sequence 18, Appl
5	1732.7	95.0	1163	16 US-10-810-653-18	Sequence 18, Appl
6	1637	89.8	1162	16 US-10-633-423-10	Sequence 10, Appl
7	1637	89.8	1162	16 US-10-427-741-10	Sequence 10, Appl
8	1622.9	89.0	1163	15 US-10-267-502-431	Sequence 431, App
9	1603.3	87.9	373	9 US-09-789-386-6	Sequence 6, Appl
10	1603.3	87.9	373	9 US-09-765-205-6	Sequence 6, Appl
11	1603.3	87.9	373	9 US-09-893-348-24	Sequence 24, Appl

12	1603.3	87.9	373	14 US-10-060-036-72	Sequence 72, Appl
13	1603.3	87.9	373	15 US-10-408-967-8	Sequence 8, Appl
14	1603.3	87.9	373	16 US-10-810-653-24	Sequence 24, Appl
15	1603.3	87.9	373	17 US-10-347-663-6	Sequence 6, Appl
16	1595.3	87.5	373	16 US-10-466-258-4	Sequence 4, Appl
17	1518.4	83.3	1192	9 US-09-789-386-2	Sequence 2, Appl
18	1518.4	83.3	1192	9 US-09-758-140-6	Sequence 6, Appl
19	1518.4	83.3	1192	9 US-09-893-348-23	Sequence 23, Appl
20	1518.4	83.3	1192	9 US-09-972-599A-6	Sequence 6, Appl
21	1518.4	83.3	1192	14 US-10-060-036-71	Sequence 71, Appl
22	1518.4	83.3	1192	15 US-10-267-502-429	Sequence 429, App
23	1518.4	83.3	1192	16 US-10-327-213-9	Sequence 9, Appl
24	1518.4	83.3	1192	16 US-10-466-258-9	Sequence 9, Appl
25	1518.4	83.3	1192	16 US-10-810-653-23	Sequence 23, Appl
26	1511.4	82.9	1192	15 US-10-408-967-7	Sequence 7, Appl
27	921	50.5	199	9 US-09-893-348-21	Sequence 21, Appl
28	921	50.5	199	16 US-10-810-653-21	Sequence 21, Appl
29	904	49.6	199	9 US-09-893-348-25	Sequence 25, Appl
30	904	49.6	199	15 US-10-660-946-1	Sequence 1, Appl
31	904	49.6	199	16 US-10-810-653-25	Sequence 25, Appl
32	897	49.2	199	15 US-10-408-967-9	Sequence 9, Appl
33	895	49.1	199	11 US-09-978-360A-467	Sequence 467, App
34	864	47.4	199	16 US-10-466-258-11	Sequence 11, Appl
35	826.3	45.3	776	15 US-10-660-946-5	Sequence 5, Appl
36	826.3	45.3	776	15 US-10-267-502-430	Sequence 430, App
37	826.3	45.3	776	16 US-10-723-860-1481	Sequence 1481, App
38	823.2	45.2	780	15 US-10-267-502-432	Sequence 432, App
39	807.4	44.3	777	14 US-10-205-219-93	Sequence 93, Appl
40	790	43.3	356	15 US-10-660-946-6	Sequence 6, Appl
41	687.7	37.7	593	15 US-10-108-260A-2892	Sequence 2892, App
42	683	37.5	208	15 US-10-660-946-7	Sequence 7, Appl
43	679	37.2	266	15 US-10-276-774-2330	Sequence 2330, App
44	672.9	36.9	269	14 US-10-106-698-6222	Sequence 6222, App
45	669	36.7	267	14 US-10-205-194-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match 99.7%; Score 1817; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 8.9e-55;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5
 US-10-810-653-18
 ; Sequence 18, Application US/10810653
 ; Publication No. US20040253218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
 ; FILE REFERENCE: EIS-SCHWARTZ=2A
 ; CURRENT APPLICATION NUMBER: US/10/810,653
 ; CURRENT FILING DATE: 2004-03-29
 ; PRIOR APPLICATION NUMBER: US/09/893,348
 ; PRIOR FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 09/218,277
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 1163
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-810-653-18

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:16:50 ; Search time 113.842 Seconds
(without alignment)
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Title: US-09-830-972-2-FUSED

Perfect score: 1823

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Total number of hits satisfying chosen parameters: 2105692

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Post-processing: Minimum Match 0%
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- 8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1817	99.7	360	3	AAY71383 Rat neuro
3	1817	99.7	360	5	AB881076 Rat neuro
4	1812.9	99.4	361	3	AAY71385 Alternati
5	1808.1	99.2	379	7	AD885283 Rat fooc
6	1732.7	95.0	1163	3	AAY71310 Rat neuro
7	1732.7	95.0	1163	3	AAY71384 Alternati
8	1732.7	95.0	1163	5	AB881074 Rat neuro
9	1732.7	95.0	1163	8	AD026399 Rat trunc
10	1732.7	95.0	1163	8	ADP45572 Rat NogoA
11	1726.7	94.7	1162	3	AAY71557 Rat Nogo
12	1637	89.8	1162	8	AD789537 Mus muscu
13	1622.9	89.0	1163	8	AD008105 Mouse pol
14	1603.3	87.9	373	3	AAY53624 A bone ma
15	1603.3	87.9	373	3	AAY56969 Human MAG
16	1603.3	87.9	373	3	AB24242 Human Nogo
17	1603.3	87.9	373	4	AB882350 Human Nogo
18	1603.3	87.9	373	5	AA47954 Human RIN
19	1603.3	87.9	373	5	ABF68601 Human pan
20	1603.3	87.9	373	5	AB881079 Human neu
21	1603.3	87.9	373	7	AD163044 Human apo
22	1603.3	87.9	373	7	ADK67503 Human RIN
23	1603.3	87.9	373	8	ADP67235 Human Nogo
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27	1518.4	83.3	1192	4	AAU04591 Human Nogo
28	1518.4	83.3	1192	5	ABG30938 Human Nogo
29	1518.4	83.3	1192	5	ABP68600 Human pan
30	1518.4	83.3	1192	5	AB881078 Human neu
31	1518.4	83.3	1192	5	ABR59667 Human Nogo
32	1518.4	83.3	1192	8	AD008103 Human pol
33	1518.4	83.3	1192	8	ADP45551 Human Nogo
34	1518.4	83.3	1192	8	ADP67234 Human Nogo
35	1518.4	83.3	1192	8	ADP13966 Human Nogo
36	1511.4	82.9	1192	7	ADK67502 Human RIN
37	1511.4	82.9	1192	8	AD026400 Human tru
38	1510.8	82.9	1178	3	AAV71311 Human neu
39	1263	69.3	360	4	AAE03987 Human gen
40	1237.7	67.9	1246	4	AAU03328 Novel hum
41	1204.7	66.1	291	4	AAW93484 Human pro
42	1204.7	66.1	291	8	ADL31138 Human pol
43	1013.8	55.6	973	8	ADQ16420 Fusion pr
44	1012.1	55.5	983	6	ABU11573 Human MDD
45	1010.8	55.4	893	3	AAY95012 Human sec

ALIGNMENTS

RESULT 1

AAV71558
ID AAY71558 standard; protein; 359 AA.

XX AC AAY71558;

XX DT 02-NOV-2000 (first entry)

XX DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.

XX KW Rat; neurite growth inhibitor; Nogo A: neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

XX OS Rattus sp.

XX FH Key Location/Qualifiers
XX Region 1..171

XX FT /note= "Corresponds to residues 1-171 of rat Nogo A
XX Region protein shown in AAY71310"

XX FT /note= "Corresponds to residues 975-1162 of rat Nogo A
XX Region protein shown in AAY71310"

XX WO200031235-A2.

XX PD 02-JUN-2000.

XX PF 05-NOV-1999; 99WO-US026160.

XX PR 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

XX (CHEN/) CHEN M S.

XX PI Schwab ME, Chen MS;

XX DR WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.

XX PS Example; Page; 122pp; English.

XX XX

ID ADB85283 standard; protein; 379 AA.
AC ADB85283;
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DT 04-DEC-2003 (first entry)
XX
DE Rat foocen-m2 reticulon SEQ ID NO:164.
XX
KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
KW protease; enzyme; analgesic; gene therapy; pain; diabetes.
XX
OS Rattus norvegicus.
XX
PN EP1284297-A2.
XX
PD 19-FEB-2003.
XX
PF 26-JUL-2002; 2002EP-00255228.
XX
PR 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002880.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brooksbank RA, Dixon AK, Lee K, Pincock RD;
XX
DR WPI; 2003-364994/35.
DR N-PSDB; ADB85284.
XX
PT Use of gene sequence that is down-regulated in response to streptozocin-
PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in
PT screening of compounds for treating or diagnosing pain.
XX
PS Disclosure; Page 239-240; 256pp; English.
XX
CC The invention relates to a novel isolated gene sequence that is down-
CC regulated in the spinal cord in response to streptozocin-induced
CC diabetes, or comprising, hybridising or having at least 80% sequence
CC identity to a sequence whose expression products are kinases,
CC phosphatases, ion channel proteins, receptors, transporters, G-protein
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
CC given in the specification. A gene of the invention has analgesic
CC activity, and may have a use in gene therapy. The gene sequences, vector,
CC host cell, animal, polypeptide and antibody are useful for screening of
CC compounds for diagnosing or treating pain. The kits are useful for
CC simultaneous, separate or sequential detecting and/or quantifying down-
CC regulation of a gene sequence in the spinal cord of a mammal in response
CC to streptozocin-induced diabetes. The compound or pharmaceutical
CC composition is useful as a medicament for treating or diagnosing pain.
CC The present sequence represents a protein encoded by a gene of the
CC invention.
XX
SQ Sequence 379 AA;

Query Match 99.2%; Score 1808.1; DB 7; Length 379;
Best Local Similarity 94.7%; Pred. No. 7.5e-65;
Matches 359; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MEDIDQSSIVSSSTDSPPPPAPKVFYVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60
DB 1 MEDIDQSSIVSSSTDSPPPPAPKVFYVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60

QY 61 PAAGLSAAVPPAAAPLLDFSSDVPAPRGLPAAPAPRQPSWERSPPAAPAPSLP 120
DB 61 PAAGLSAAVPPAAAPLLDFSSDVPAPRGLPAAPAPRQPSWERSPPAAPAPSLP 120

QY 121 PAAAVLPKLPDEDPAPPPPPAGASPLAEPAPSTPAAPKRGSG----- 170
DB 121 PAAAVLPKLPDEDPAPPPPPAGASPLAEPAPSTPAAPKRGSGVDETLFALP 180

QY 171 -----SSVVLLIYWRDIKKTGVFGASIFLLISLTVFSIVSVTAYIALALLSVTIS 221
:|||||

Db 181 RASEPVISSAVVLLIYWRDIKKTGVFGASIFLLISLTVFSIVSVTAYIALALLSVTIS 240
QY 222 PRIYKGVIAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVD 281
|||
Db 241 PRIYKGVIAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVD 300
QY 282 DLVDSLKFAVLMMVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV 341
|||
Db 301 DLVDSLKFAVLMMVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV 360
QY 342 KDAMAKIOAKIPGLKPKAD 360
|||
Db 361 KDAMAKIOAKIPGLKPKAD 379

RESULT 6
AAY71310
ID AAY71310 standard; protein; 1163 AA.
XX
AC AAY71310;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Inhibitory-site 1..171 /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30 /note= "Casein kinase II site"
FT Region 31..58 /note= "Acidic region"
FT Region 31..57 /note= "Region specifically described in claim 16"
FT Region 172..259 /note= "This region is not essential for inhibitory activity"
FT Modified-site 233 /note= "Protein kinase C (PKC) site"
FT Modified-site 242..244 /note= "Asn is N-glycosylated"
FT Modified-site 291 /note= "Protein kinase C (PKC) site"
FT Modified-site 295 /note= "Protein kinase C (PKC) site"
FT Misc-difference 404 /note= "Encoded by TTG"
FT Modified-site 436 /note= "Protein kinase C (PKC) site"
FT Modified-site 468..470 /note= "Asn is N-glycosylated"
FT Modified-site 484 /note= "Protein kinase C (PKC) site"
FT Modified-site 488 /note= "Protein kinase C (PKC) site"
FT Modified-site 502 /note= "Casein kinase II site"
FT Inhibitory-site 542..722
FT Modified-site 576 /note= "Casein kinase II site"
FT Peptide 623..640 /note= "used as immunogen to generate antibody AS 472"
FT Modified-site 626

FT /note= "Protein kinase C (PKC) site"
 FT 694..696
 FT /note= "Asn is N-glycosylated"
 FT 715
 FT /note= "Casein kinase II site"
 FT 762..1163
 FT /note= "used as immunogen to generate antibody AS Bruna"
 FT 784
 FT /note= "Protein kinase C (PKC) site"
 FT 821
 FT /note= "Protein kinase C (PKC) site"
 FT 850
 FT /note= "Protein kinase C (PKC) site"
 FT 855
 FT /note= "Protein kinase C (PKC) site"
 FT 863
 FT /note= "Casein kinase II site"
 FT 868
 FT /note= "Protein kinase C (PKC) site"
 FT 893
 FT /note= "Protein kinase C (PKC) site"
 FT 912..914
 FT /note= "Asn is N-glycosylated"
 FT 925..927
 FT /note= "Asn is N-glycosylated"
 FT 954
 FT /note= "PKC and casein kinase II sites"
 FT 956
 FT /note= "PKC and casein kinase II sites"
 FT 975..1162
 FT /note= "This region is not essential for inhibitory activity"
 FT 976..1163
 FT /note= "C-terminal common region found in Nogo A, B and C isoforms"
 FT 988..1023
 FT /label= Transmembrane domain
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"
 FT 1024
 FT /note= "Protein kinase C (PKC) site"
 FT 1071..1073
 FT /note= "Asn is N-glycosylated"
 FT 1073
 FT /note= "Protein kinase C (PKC) site"
 FT 1089
 FT /note= "Protein kinase C (PKC) site"
 FT 1090..1125
 FT /label= Transmembrane domain
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"
 FT 1141..1143
 FT /note= "Asn is N-glycosylated"
 FT 1143
 FT /note= "Protein kinase C (PKC) site"
 FT WO200031235-A2.
 FT 02-JUN-2000.
 FT 05-NOV-1999; 99WO-US026160.
 FT 06-NOV-1998; 98US-0107446P.
 FT (SCHW/) SCHWAB M E.
 FT (CHEN/) CHEN M S.
 FT Schwab ME, Chen MS;
 FT WPI: 2000-400052/34.
 FT N-PSDB; AAD01173.
 FT Nogo proteins and nucleic acids useful for treating neoplastic disorders

PT of the central nervous system and inducing regeneration of neurons.
 XX Claim 3; Fig 2A; 122pp; English.
 CC The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing RO18U37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID NO: 2 is stated to be the same as the sequence shown in Fig. 13 (see AAY71384) of the specification. However, this sequence does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers
 XX Sequence 1163 AA;

Query Match 95.0%; Score 1732.7; DB 3; Length 1163;
 Best Local Similarity 31.0%; Pred. No. 5.7e-61;
 Matches 360; Conservative 0; Mismatches 0; Indels 803; Gaps 1;
 QY 1 MEDIDQSLVSSSTDSPPRPAPKQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 DB 1 MEDIDQSLVSSSTDSPPRPAPKQVTPPEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 QY 61 PAAGLSAAAVPAAAPLLDFSSDVPAPRGPAPAPAPAPAPAPAPAPAPAPAPAPSLP 120
 DB 61 PAAGLSAAAVPAAAPLLDFSSDVPAPRGPAPAPAPAPAPAPAPAPAPAPAPAPSLP 120
 QY 121 PAAVLPKLPEDPEPPAPPPPPAGASPLAEPAPSTPAAPKRGSGS----- 171
 DB 121 PAAVLPKLPEDPEPPAPPPPPAGASPLAEPAPSTPAAPKRGSGSVDETLFAIP 180
 QY 172 ----- 171
 DB 181 AASEPVISSAEKIMDLMEQPGNTVSSQEDPFPVLLTAASLPSTVTSFKEHGYL 240
 QY 172 ----- 171
 DB 241 GNLSAVSSSEGTIBETLINEASKELPERATNPFVNRDLAEFSELEYSEMGSFPGSPKGES 300
 QY 172 ----- 171
 DB 301 AILVENTKEVIVRSKOKEDLVCSAALHSPQSPVGKEDRVVSPKTDWIDFNEMQMSVVA 360
 QY 172 ----- 171
 DB 361 PVREYADFKPEQAWVEVKDTYEGSRDVLAAANVESKVDKCIEDSLKSLGKDSGR 420
 QY 172 ----- 171
 DB 421 NEDASFPSTPEPVKDSRRAYITCASFTSATESTTANTPFLLEDHTSENKTDKIEERKA 480
 QY 172 ----- 171
 DB 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDLTKVTEAAVSNMPEGLTDLVQACESEL 540

QY	172	-----	171	FT	Region	172..259	
Db	541	NEATGKIAYETKVDLVQTSIAQESLYTAQLCPSEAEATPSPVLPDIWMEAPLNSL	600	FT	/note= "This region is not essential for inhibitory activity"		
QY	172	-----	171	FT	Misc-difference	223	
Db	601	LPSAGASVVQPSVSPLEAPPVSDYSIKLEPENPPPEAMNVALKALGTKEIKEPSPF	660	FT	/label= Unknown		
QY	172	-----	171	FT	/note= "There is Leu at this position in the sequence shown in AAY71310"		
Db	661	NAAVQTEAPYISACDLIKETKLTSPSPDFSNYSIAKFEKSVPEHAELVEDSSPSE	720	FT	233	"Protein kinase C (PKC) site"	
QY	172	-----	171	FT	242..244		
Db	721	PVDLFSDDSIPEVPQTEAEAVMLKESLTVSETVAQHKEERLSASPSQLGPKYLESPQ	780	FT	/note= "Asn is N-glycosylated"		
QY	172	-----	171	FT	291	"Protein kinase C (PKC) site"	
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEERENTAIYSNDLLSSKEDKIKESETFSDSSPIE	840	FT	295	"Protein kinase C (PKC) site"	
QY	172	-----	171	FT	404	"Protein kinase C (PKC) site"	
Db	841	IIDEPTFVSAXDPSKLAKEYTDLEVSDKSEIANIQSGADSLPCLLPCLDLSFKNIYPK	900	FT	/note= "There is Ile at this position in the sequence shown in AAY71310"		
QY	172	-----	171	FT	436		
Db	901	DEVHVSDFSENSSVSKASISPSNVSALEPQTEMGSIYKSKSLTKAEAKKLPSDTEKED	960	FT	/note= "Protein kinase C (PKC) site"		
QY	172	-----	171	FT	468..470		
Db	961	RSLSAVLSNELSKTSVDDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLS	1020	FT	/note= "Asn is N-glycosylated"		
QY	218	VTISFRIYKGVIOAQKSDGHPFRAYLSEVAISEELVQKYSNGALGHVNSTIKELRRL	277	FT	469		
Db	1021	VTISFRIYKGVIOAQKSDGHPFRAYLSEVAISEELVQKYSNGALGHVNSTIKELRRL	1080	FT	/label= Unknown		
QY	278	FLVDDLVDLSKFAVLMMWFTYTYGALFNGLTILILALISLFSIPVIYERHQVIDHYLGIA	337	FT	/note= "There is Lys at this position in the sequence shown in AAY71310"		
Db	1081	FLVDDLVDLSKFAVLMMWFTYTYGALFNGLTILILALISLFSIPVIYERHQVIDHYLGIA	1140	FT	484	"Protein kinase C (PKC) site"	
QY	338	NKSVKDMAKIOAKIPGLKRRKAD	360	FT	488	"Protein kinase C (PKC) site"	
Db	1141	NKSVKDMAKIOAKIPGLKRRKAD	1163	FT	502	"Protein kinase C (PKC) site"	
RESULT 7				FT	542..722		
AAV71384				FT	/note= "Casein kinase II site"		
ID	AAV71384	standard; protein; 1163 AA.		FT	576		
XX				FT	623..640		
AC	AAV71384;			FT	/note= "used as immunogen to generate antibody AS Bruna"		
XX				FT	661	"Protein kinase C (PKC) site"	
DT	02-NOV-2000	(first entry)		FT	694..696		
XX				FT	/note= "There is Asn at this position in the sequence shown in AAY71310"		
DE		Alternative version of rat neurite growth inhibitor Nogo A.		FT	715		
XX				FT	/note= "Asn is N-glycosylated"		
KW		Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;		FT	762..1163		
KW		central nervous system; neoplastic disease; antiproliferative; glioma;		FT	/note= "used as immunogen to generate antibody AS Bruna"		
KW		antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;		FT	784	"Protein kinase C (PKC) site"	
KW		degenerative nerve disease; Alzheimer's disease; Parkinson's disease;		FT	820		
KW		hyperproliferative disorder; benign dysproliferative disorder; diagnosis;		FT	/note= "There is Leu at this position in the sequence shown in AAY71310"		
KW		psoriasis; tissue hypertrophy; neuronal regeneration; treatment;		FT	821	"Protein kinase C (PKC) site"	
XX		structural plasticity; screening.		FT	850		
OS		Rattus sp.		FT	/note= "Protein kinase C (PKC) site"		
XX				FT	855	"Protein kinase C (PKC) site"	
PH		Key		FT	863	"Protein kinase C (PKC) site"	
FT		Inhibitory-site 1..171		FT	/note= "Casein kinase II site"		
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"		FT	868	"Protein kinase C (PKC) site"	
FT		Modified-site 30		FT	893		
FT		/note= "Casein kinase II site"		FT	/note= "Protein kinase C (PKC) site"		
FT		Region 31..58		FT	912..914		
FT		/note= "Acidic region"		FT	/note= "Asn is N-glycosylated"		
FT				FT	925..927		
FT				FT	/note= "Asn is N-glycosylated"		
FT				FT	954	"PKC and casein kinase II sites"	
FT				FT	/note= "PKC and casein kinase II sites"		

FT	Region	975..1162 /note= "This region is not essential for inhibitory activity"
FT	FT	976..1163
FT	Region	/note= "C-terminal common region found in Nogo A, B and C isoforms"
FT	Domain	988..1023 /label= Transmembrane domain /note= "C-terminal hydrophobic region"
FT	Modified-site	1024 "Protein kinase C (PKC) site"
FT	Modified-site	1071..1073 /note= "Asn is N-glycosylated"
FT	Modified-site	1073 /note= "Protein kinase C (PKC) site"
FT	Modified-site	1089 /note= "Protein kinase C (PKC) site"
FT	Domain	1090..1125 /label= Transmembrane domain /note= "C-terminal hydrophobic region"
FT	Modified-site	1141..1143 /note= "Asn is N-glycosylated"
FT	Modified-site	1143 /note= "Protein kinase C (PKC) site"
XX	WO200031235-A2.	
XX	PN	
XX	PD	02-JUN-2000.
XX	PP	05-NOV-1999; 99WO-US026160.
XX	PR	06-NOV-1998; 98US-0107446P.
XX	PA	(SCHW/) SCHWAB M E. (CHEN/) CHEN M S.
XX	PI	Schwab ME, Chen MS;
XX	DR	WPI; 2000-400052/34.
XX	Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.	
XX	Claim 3; Fig 13; 122pp; English.	
CC	The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AA71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers	
XX	Sequence 1163 AA;	
Query Match	95.0%; Score 1732.7; DB 3; Length 1163;	
Best Local Similarity	31.0%; Pred. No. 5.7e-61;	
Matches 360; Conservative	0; Mismatches 0; Indels 803; Gaps 1;	

RESULT 11
ID AAY71557 standard; protein; 1162 AA.
AC AAY71557;
DT 02-NOV-2000 (first entry)
XX Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
XX
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; benign dysproliferative disorder; treatment;
KW structural plasticity; screening; mutant; mutation.
XX
OS Rattus sp.
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Example; Page; 122pp; English.
XX
XX The patent relates to neurite growth inhibitor Nogo which is free of all
XX central nervous system (CNS) myelin material with which it is natively
XX associated. Nogo proteins and fragments displaying neurite growth
XX inhibitory activity are used in the treatment of neoplastic disease of
XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
XX ependymoma, pinealoma, haemangioblastoma, acoustic neuroma,
XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
XX Therapeutics which promote Nogo activity can be used to treat or prevent
XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
XX used to inhibit production of Nogo protein to induce regeneration of
XX neurons or to promote structural plasticity of the CNS in disorders where
XX neurite growth, regeneration or maintenance are deficient or desired. The
XX animal models can be used in diagnostic and screening methods for
XX predisposition to disorders and to screen for or test molecules which can
XX treat or prevent disorders or diseases of the CNS. The present sequence
XX is a truncated form of rat Nogo A protein shown in AAY71310, which is
XX used in the construction of mutant Nogo-A. Nogo-A is composed of His-
XX tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
XX used for mapping the inhibitory sites of Nogo protein. Major inhibitory
XX region was identified in the Nogo A sequence from amino acids 172-974,
XX particularly amino acids 542-722. In addition, N-terminal region 1-171
XX was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
XX present sequence is not given in the specification but is derived from
XX rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
XX in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
XX However, the specification does not include sequences for these SEQ ID
XX numbers
XX Sequence 1162 AA;

Query Match 94.7%; Score 1726.7; DB 3; Length 1162;
Best Local Similarity 30.9%; Pred. No. 1e-60;
Matches 359; Conservative 0; Mismatches 0; Indels 803; Gaps 1;
QY 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60
DB |||||
QY 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDELEVLERK 60
DB |||||
QY 61 PAAGLSAAAVPAAAPLDDFSSDSVPPAPRGPLPAAPPAAPROPSKERSPAAAPSP 120
DB |||||
QY 61 PAAGLSAAAVPAAAPLDDFSSDSVPPAPRGPLPAAPPAAPROPSKERSPAAAPSP 120
DB |||||
QY 121 PAAAVLPKLPEDDEPPAPPPPPAGASPLAEPAAPESTPAAPKRRSGS 171
DB |||||
QY 121 PAAAVLPKLPEDDEPPAPPPPPAGASPLAEPAAPESTPAAPKRRSGSVDLTFALP 180
DB |||||
QY 172 ----- 171
DB 181 AASEFVIPSSAEKIMDLMEQFGNTVSSQEDFPVSVLLETAASLPSLSTVSKHEGYL 240
QY 172 ----- 171
DB 241 GNLGAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFGKSGKES 300
QY 172 ----- 171
DB 301 AILVENTKEEVIVRSKDKEDLVCSAALHSQESPVGKEDRVVSPKTMDFNMQMSVVA 360
QY 172 ----- 171
DB 361 PVREYADFKPFEQAWEVKDTYEGSRDVLAAANVESKVDKRCIEDSLQKSLGKDSGR 420
QY 172 ----- 171
DB 421 NEDASFPSTPBPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDKKEERKA 480
QY 172 ----- 171
DB 481 QIITEKTSKPTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTDLVQEAESSEL 540
QY 172 ----- 171
DB 541 NEATGTKIAYETKVDLVQVTSIAQESLYTAQLCPSFEAEATPSPVLDPDIMEAPLNSL 600
QY 172 ----- 171
DB 601 LPSAGASVVQPSVPLEAPPVVSYSIKLEPENPPPYEAMNVALKALGTKEGKEPSF 660
QY 172 ----- 171
DB 661 NAAVQETEAPYISIACDLIKETLSTEPSPDFSNYSYSEIAKPEKSVPEHAELVEDSSPSE 720
QY 172 ----- 171
DB 721 PVDLFSDSDSIPEVPQTQBEAVMLKESLTVSETVAQHKEERLSASPOELGKPYLESFQP 780
QY 172 ----- 171
DB 781 NLHSTKDAASNDIPTLTKEKISLOMEEFNTAIYSNDDLLSSKEDKIKESFTSDSSPIE 840
QY 172 ----- 171
DB 841 IIDEFPTFVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLELPCDLSPKNIYPK 900
QY 172 ----- 171
DB 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEGSIKSVKSLTKAEAKKLPSSTEKED 960
QY 172 -----SVVDLLYWRDIKKTGVVFGASLFLLLSLTIVFSIVSVTAYIALALLS 217
DB 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTIVFSIVSVTAYIALALLS 1020
QY 218 VTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRL 277

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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:29:31 ; Search time 24.9653 Seconds
(without alignments)
1387.446 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIDQSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826.3	45.3	776	2 A46583	neuroendocrine-spe
2	683	37.5	208	2 I60904	neuroendocrine-spe
3	669	36.7	267	2 A60021	tropomyosin-relate
4	437.7	24.0	2484	2 T26216	hypothetical prote
5	427.4	23.4	2607	2 T28215	hypothetical prote
6	337.5	18.5	222	2 T26213	hypothetical prote
7	272.1	14.9	786	2 A35466	progesterone recep
8	266.9	14.6	1173	2 T31421	C-terminal domain-
9	265.5	14.6	1611	2 T38236	hypothetical prote
10	258.5	14.2	1058	2 T13286	capuccino gene pr
11	257.8	14.1	1100	2 JC8033	leukocyte formin p
12	257.5	14.1	1206	2 S24407	formin isoform IV
13	256.4	14.1	3530	2 A59266	unconventional myo
14	254.9	14.0	1468	2 S11515	formin - mouse
15	254.7	14.0	716	2 T26998	hypothetical prote
16	253.8	13.9	760	2 F86387	probable Pto kinas
17	253.2	13.9	929	2 C96623	hypothetical prote
18	253.2	13.9	1255	2 T13065	diaphanous protein
19	252.2	13.8	2157	2 S71461	proline-rich prote
20	251.9	13.8	1201	2 G86441	unknown protein li
21	250.9	13.8	1015	2 JC6552	DNA topoisomerase
22	250.2	13.7	907	2 E96636	hypothetical prote
23	246.4	13.5	1657	2 T19536	hypothetical prote
24	246	13.5	1522	2 T39371	transcription regu
25	245.8	13.5	645	2 A71416	hypothetical prote
26	245.4	13.5	1460	1 ADEBIF	immediate-early pr
27	245.2	13.5	3511	2 A59295	unconventional myo
28	245.1	13.4	710	2 D96728	hypothetical prote
29	244.7	13.4	465	2 G02738	FRAC-4 - human

30	244.3	13.4	1064	2 T13963	formin related pro
31	242.7	13.3	1533	2 T00344	hypothetical prote
32	242.1	13.3	1375	2 S48375	hypothetical prote
33	241.9	13.3	1213	2 A58198	serine/proline-ric
34	241.7	13.3	3938	2 T42761	Bassoon protein -
35	241.1	13.2	775	1 EDBE11	immediate-early pr
36	240.9	13.2	980	2 G75523	probable cell divi
37	240.6	13.2	1634	2 T25517	hypothetical prote
38	240.5	13.2	1446	1 A45344	immediate-early pr
39	238.9	13.1	731	2 T04455	hypothetical prote
40	238.5	13.1	1047	2 A55617	masquerade precurs
41	238.5	13.1	1420	2 T37781	probable cytoskele
42	238.4	13.1	7962	2 I38346	elastic titin - hu
43	238	13.1	3149	1 QQBE8	BPL1 protein - hu
44	237.6	13.0	933	1 QRHUP	progesterone recep
45	237.5	13.0	980	2 S54986	regulatory protein

ALIGNMENTS

RESULT 1

A46583

N:Contains: neuroendocrine-specific protein, splice form A - human

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V&

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: A46583

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-776 <ROI>

A:Cross-references: UNIPROT:Q16799; GB:I10333; NID:g307306; PIDN:AAAS9950.1; PID:g307307

A:Accession: I60903

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 421-776 <ROE2>

A:Cross-references: GB:I10334; NID:g307308; PIDN:AAAS9951.1; PID:g307309

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 45.3%; Score 826.3; DB 2; Length 776;
Best Local Similarity 27.7%; Pred. No. 6.7e-20;
Matches 195; Conservative 52; Mismatches 91; Indels 367; Gaps 17;

QY	10	VSSSTDS-----PPR-----	19
DB	85	VSSAMDTFTSKDGGSCYTSLSIDICYPQEDSTYFTGILQKENGHVITSESPEELG	144
QY	20	PPP-----	34
DB	145	TPGSLPDPVPGIESRGLFSSDSGIEMTPAESTENVKNILADPDQMKAEYKYIDITRPEE	204
QY	35	EDEEEDEDEED-----DED-----	50
DB	205	VKHQSHPELEDKOLDPFNKDIDISIKPEGVREPKAPVGEKIKHLLLEESTPAPYI	264
QY	51	-----LEELE-----	55
DB	265	DDLSEQRRAPIITFPVKITLIEIPSVETTTQETKPEKQDICKLPSPDTVFTVTVSEPE	324
QY	56	-----VLERKPAAGLS-----	66
DB	325	DDSPGSITPPSSGTEPSAAESQKGKSGISEDELITAIKEAKGLSYETAENPRPVGLADRP	384
QY	67	---AAAVPAAAPLLDFSSDSV-----PPA 89	

Dbb 385 EVKARSGPTTIPSP-LDHEASSAESGDSIEILVSEDPMAEDALPSGVYSGHVGPPPS 443

Qy 90 PRGPL-----PAAPPA----- 100

Dbb 444 PASPSIQSYLLREERAEALDSLIIESDCASSASRESPKREQDSPMPKPSALDAIRETG 503

Qy 101 --APRQPS-----WERSPAAPAPSLPPA-----AAVLPSPKPEDD-----E 135

Dbb 504 VRAERAPSRRLGAEPSFLDYSPTEPGPGPLPGDGALEPETMPLPRK-PEEDSSNQ 562

Qy 136 PPARPPPPPPACASPLAEPAPSPSTPAAPKRGSSVVLDLYWDIKKTVGVFGASFL 195

Dbb 563 SPAATKGGPLG-----PGAPPLFLNKKQ-----AIDLLYWRDIKQTGIVFGSFL 611

Qy 196 LLSLVFVSIVSVTAYIALALLSVTISFRIYKVIQAIQKSDGHPFRAYLSEVAISEEL 255

Dbb 612 LFSLTQFVSVVAVIALAALSATISFRIYKSVLQAVQKTDGHPFKAYLEIYTLSEQ 671

Qy 256 VQKYSNSALGHVNSTIKELRRLFLVDDLSLKFPAVLMMVFTYVVGALFNGLTLLILALIS 315

Dbb 672 IOKYTDCLQFYVNSTKELRRLFLVODLVDSLKFPAVLMMVFTYVVGALFNGLTLLMAVVS 731

Qy 316 LFSIPVIYERHQVQIDHYGLANKSVKDMAKIQKIPGLKRAKAD 360

Dbb 732 MFTLEPVVYVKHQADIQDYLGLVTRTHINAVAVKIQKIPGAKRHA 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16799; GB:I10335; NID:G307310; PIDN:AAA59952.1; PID:G307311

C:Genetics:

A:Gene: GDB:R1N1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 37.5%; Score 683; DB 2; Length 208;

Best Local Similarity 67.4%; Pred. No. 1.8e-16;

Matches 128; Conservative 31; Mismatches 31; Indels 0; Gaps 0;

Qy 171 SSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKVIQ 230

Dbb 19 SQAILLLYWRDIKQTGIVFGSFLLLSLTFQSVSVVAYIALAALSATISFRIYKSVLQ 78

Qy 231 AIQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLSLKFA 290

Dbb 79 AVQKTDEGHPFKAYLEIITLSQEIQKYTDCQLQYVNSTLKELRRLFLVQDLVDSLKA 138

Qy 291 VLMVFTYVVGALFNGLTLLILALISLSPFIPIYERHQVQIDHYGLANKSVKDMAKIQA 350

Dbb 139 VLMWLLTYVVGALFNGLTLLMAVVSMTPLPVVYVKHQADIQDYLGLVTRTHINAVAKIQA 198

Qy 351 KIPGLKRAKAD 360

Dbb 199 KIPGAKRHA 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C:Accession: A60021

R:Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A:Reference number: A60021; MUID:91278684; PMID:1647480

A:Accession: A60021

A:Molecule type: mRNA

A:Residues: 1-267 <WIE>

A:Cross-references: EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PID:9456550

C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 36.7%; Score 669; DB 2; Length 267;

Best Local Similarity 66.7%; Pred. No. 1e-15;

Matches 124; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

Qy 171 SSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKVIQ 230

Dbb 10 SQAILLLYWRDIKQTGIVFGSFLLLSLTFQSVSVVAYIALAALSATISFRIYKSVLQ 69

Qy 231 AIQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLSLKFA 290

Dbb 70 AVQKTDEGHPFKAYLEIITLSQEIQKYTDCQLQYVNSTLKELRRLFLVQDLVDSLKA 129

Qy 291 VLMVFTYVVGALFNGLTLLILALISLSPFIPIYERHQVQIDHYGLANKSVKDMAKIQA 350

Dbb 130 VLMWLLTYVVGALFNGLTLLMAVVSMTPLPVVYVKHQADIQDYLGLVTRTHINAVAKIQA 189

Qy 351 KIPGLK 356

Dbb 190 KIPGAR 195

RESULT 4

T26216

hypotheical protein W06A7.3c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26216

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26216

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2484 <WIL>

A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3c

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 24.0%; Score 437.7; DB 2; Length 2484;

Best Local Similarity 14.8%; Pred. No. 1.5e-05;

Matches 135; Conservative 77; Mismatches 138; Indels 563; Gaps 21;

Qy 1 MEDIDQSSL-----VSSST----- 14

Dbb 1566 MEVTESEISEMAQVSESTCTPIPEPLADLKLPEVDEDEKTEPEPEVPVGVQVERIPIEV 1625

Qy 15 ----DSPPRPPAPKYQF--VTEPEDE----- 35

Dbb 1626 EQAPTIPQPPRAPKSELPAKPLDSDSKSRVFAPLNKLGRTYSEBQQKELVESLERP 1685

Qy 36 -----ED-----EEDEDE----- 44

Dbb 1686 LTIITQOKPEKPTEDIGALSPLSPNTLAEEVPMQSVPHSPQSKQSEIALSEII 1745

Qy 45 -----EEDDELELEVL----- 57

Dbb 1746 EEPQAMKEVKEVPSAPEKONESLEAPEIINEPIRRVLVETKIMGPGKSLNEDDDDDG 1805

Qy 58 ----- 57

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Db 1806 SECLDSIGLSERTIQRFTNTSIDDPSIRRDSPSSISSFGDRKFRRTAENIRQDILLPQOS 1865
QY 58 -----DSPRRPPPAKYQF--VTEPEDE-----ERKPA----- 63
Db 1866 SVSQYLRSSPNPSQQLLVNLSMDSPDLSPNAPVPGFNTAQFLKQLQEDRPSAEGSI 1925
QY 64 -----GLSAAAVPP-----ED-----EEREDE----- 44
Db 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQSVFSGSLGDDMKPGSQDDGFVFIERNEANEATL 1745
QY 73 -----AAAAPLL-----BEDDEDLEELVL----- 57
Db 1986 KKNQKMSHHNDVIEKNYFNNDNAPTAALESPIAEARKLVQDAVESAYKKQAVDSDG 2045
QY 80 -----DFSSDSVPPA-----PRGPL 94
Db 2046 EIGRELLDNVEQKIEQVKEPIVDSLHKAYDVGDFVHETVPNAVDDFVREAEKQLPESV 2105
QY 95 P-----AAPP-----AAPP-----ERKPA----- 63
Db 2106 PEKIETPEPLVDIHDVTQKHDEVDNFLRREPTPPFETDDVAPLSDDKPKQFGNQTPED 2165
QY 106 PSWER-----SPAAPAPSLPPAAAVLPKLPEDD 134
Db 2166 TTFDRKGLPTIPEEVEKAAQAQNDLDDFDPLVTSNTGAAGAAVAV--ESLTHEE 2223
QY 135 -----EPPARPPPPPPAGASPLAEPAPST-----PAAPK----- 166
Db 2224 MFGHQKFETVPRPTTP-----KDISDEDVKSTVNLGFSHHSHSPSSPHHSILKHGD 2279
QY 167 ----- 166
Db 2280 IDFTVPPCAQNAFSGEIMFLAPFVYLSCFSPFSLPLDNLNLSLVVYLSISLIH 2339
QY 167 ----- 166
Db 2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFVNLVGLNVALVGVAVSAEAYK 2399
QY 167 --RGSG-----SSVDLLIWRDIKKTGVFGASLFLLLSLTFSIVSVTAYIALALLSVTI 220
Db 2400 LTKSSGVLRKKEVLDVIYWRDAKSAIYLSLALLVFLAKYPLLTVTYTSLLALGAAA 2459
QY 221 SPRIYGVIOAKQSDGHPFRAYLESVAISEELVQKYSNSALGHVNSTIKELRRLFLV 280
Db 2460 GFRVFKVEAQIKKTDSHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKLKLVF 2519
QY 281 DDLVDSLKFAVLMVFTYVVGALFNGLLIALLISLFSIPVIYERHQVQIDHYLGLANKS 340
Db 2520 ESPLSIFGLVLSWTIYASWFSQFTLAILGLGVFSVPKYVESNQEAIDPHLATISGH 2579
QY 341 VKDAMAKTOAKIPGLK 356
Db 2580 LKNVQNIIDEKLPFLR 2595
RESULT 6
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Db 1806 SECLDSIGLSERTIQRFTNTSIDDPSIRRDSPSSISSFGDRKFRRTAENIRQDILLPQOS 1865
QY 58 -----ERKPA----- 63
Db 1866 SVSQYLRSSPNPSQQLLVNLSMDSPDLSPNAPVPGFNTAQFLKQLQEDRPSAEGSI 1925
QY 64 ----- 72
Db 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQSVFSGSLGDDMKPGSQDDGFVFIERNEANEATL 1985
QY 73 ----- 79
Db 1986 KKNQKMSHHNDVIEKNYFNNDNAPTAALESPIAEARKLVQDAVESAYKKQAVDSDG 2045
QY 80 -----DFSSDSVPPA-----PRGPL 94
Db 2046 EIGRELLDNVEQKIEQVKEPIVDSLHKAYDVGDFVHETVPNAVDDFVREAEKQLPESV 2105
QY 95 P-----AAPP-----AAPP-----ERKPA----- 105
Db 2106 PEKIETPEPLVDIHDVTQKHDEVDNFLRREPTPPFETDDVAPLSDDKPKQFGNQTPED 2165
QY 106 PSWER-----SPAAPAPSLPPAAAVLPKLPEDD 134
Db 2166 TTFDRKGLPTIPEEVEKAAQAQNDLDDFDPLVTSNTGAAGAAVAV--ESLTHEE 2223
QY 135 -----PAAP-----KRGSG- 170
Db 2224 MFGHQKFETVPRPTTP-----KDISDEDVKSTVNLGFSHHSHSPSSPHHSILKHGD 2279
QY 171 -----SSVDLLIWRDIKKTGVFGASLFLLLSLTFSIVSVTAYIALALLSVTISFR 223
Db 2280 IDFTVPPCVLDVIYWRDAKSAIYLSLALLVFLAKYPLLTVTYTSLLALGAAAGFR 2339
QY 224 IYKGVIOAKQSDGHPFRAYLESVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDL 283
Db 2340 VPKVEAQIKKTDSHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKLKLVFESP 2399
QY 284 VDSLKFAVLMVFTYVVGALFNGLLIALLISLFSIPVIYERHQVQIDHYLGLANKSVKD 343
Db 2400 LESIKFGLVLSWTIYASWFSQFTLAILGLGVFSVPKYVESNQEAIDPHLATISGH LKN 2459
QY 344 AMAKTOAKIPGLK 356
Db 2460 VQNIIDEKLPFLR 2472
RESULT 5
Hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; EMBL:Z78086; PIDN:CAB01522.2; GSPDB:GN000023; CESP:W0
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 23.4%; Score 427.4; DB 2; Length 2607;
Best Local Similarity 13.0%; Pred. No. 3.8e-05;
Matches 135; Conservative 78; Mismatches 137; Indels 686; Gaps 21;
QY 1 MEDIDQSSL-----VSSST----- 14
```


A:Experimental source: strain 972h-; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.17
A:Map position: 1

Query Match 14.6%; Score 265.5; DB 2; Length 1611;
Best Local Similarity 10.1%; Pred. No. 3.4;
Matches 131; Conservative 59; Mismatches 106; Indels 1005; Gaps 30;

```
QY 2 EDIDSSLSVS-----SSTDSPPRP----- 20
D 299 EELSKSQVAKDDDDPFVVSNTANSDEPASSKPAKPLTLNRAFSQRLNLPQPKGKSG 358
QY 21 -----PFAKYQFVTEPD-----EEDDEEEDDEE 46
D 359 ELSEQDEEYDAESDENHSPSYSTHEPESEPDQDEPSEKDDENKDVEEQEEQEEQI 418
QY 47 DDELEELEVLER----- 59
D 419 DPEAKRIALRERMAKMGSGGIMHVFGLPLGLAIPGRKNTLRLTPAKSSEAKSTNDSS 478
QY 60 -----KPAAGLS 66
D 479 PKDSSSTQTEQSNQAQAPSPKEERPLPSEPSQNPAYRDTPTPRNIMPGLM 538
QY 67 AA----- 68
D 539 SADQPIKVTSPNSADAKAIVAGPNNEBETKGPVETQETSEQQVHKTPPEKQKVLSP 598
QY 69 -----AVPPAAAPFL----- 79
D 599 PPIITNFKETILASNEAEVAPQKPSAQVTRLMAPODSSSVTPSPSTLLDPAARAKV 658
QY 80 -----DFSS----- 85
D 659 IDGIDPPKEAGAGATADVESAANSPIPTPRTWHSPDFTSKFEPIERKLPSRISVETDS 718
QY 86 V-----PPAP----- 90
D 719 IDEDKQNEVDPSTSARALPPGLRFGKVDTLASLAHDDLDLPAVPRIFSPPLPKTPSG 778
QY 91 -----RG----- 93
D 779 EFGDNEMFPKSNRVRGHQSRPSTGSQLRNVPVSVITSGRPLALPDEMASPSSIGHP 838
QY 94 LPAAPPA-----ABERQPSWERS----- 111
D 839 LPSPPPADFNLSUNDFYEPHYSLESPAPEQPSYEEESFNATVIHAPTSTATFGQHTI 898
QY 112 ----- 111
D 899 SNVATPPLKQDVTEKASPVADASATHQSSTGLTQETITQLGSNMRLPTKLTSPSNDGRKA 958
QY 112 -----PAAPAPSLPPAAAV-----L 126
D 959 SGPRPAAP-PSIPPLPVSNILSSPTSPBPKDHPSPAPLSKPVSTSPAALARVPPVKL 1017
QY 127 PSK-----LPEDDEP----- 137
D 1018 SSKAPVFLPSADAPFIVPSTAPPVPTSTPVPKSSSGAPSPAPPVPAPSPSIPSIP 1077
QY 138 ----- 137
D 1078 APSGAPPVPAPSGIPVPKPSVAAPVPKPSVAVPVPAPSPGAPPVPKPSVAAPVPVPVS 1137
QY 138 -----ARPPPPPPAGASPLAEP--AAPP----- 158
D 1138 GAPPVPKPSVAAPPVPAPSGAPPVPKPSVAAPPVPAPSGGIPVPKPAAGVPVPVPVPPSEA 1197
QY 159 -----STP----- 161
D 1198 PPVPKPSGVPPVPPPPSTAPPVPTPSAGLPPVPVPTAKAPPVPAPSPSPSVP 1257
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QY 162 -----AAPKR-----RGS 169
D 1258 SPHSNAPSPTSSSMASAPARTSVSRKSKAERHETSTSRKSKSGSGEHHHNEGHAD 1317
QY 170 GSSVVDDLLYWRDIKKTGVVFGASLFLLLSLTVF-----SIVSVTAYI----- 211
D 1318 SSSTRTSLAHODSRK-----SLRHLSRSSSRASKPSIVSTTGPFPNESFSKAPVBP 1370
QY 212 -----ALALLSVTISFRIYKGV----- 228
D 1371 ASEKWLNLNSTAVPKSVQMNDSDVLYMIKEGTDGQDKYKSVHILFPDYSQVTLTATPNPH 1430
QY 229 -----IQAIQKSGEGHPFRAYLESEVAISELQVK-----YSNGALGHVNSTIKELRLF 278
D 1431 NQNTQLSQLQALAPQAPSKARLDEEYACYGSTITLKARAYQGSVMVGDSA----- 1481
QY 279 LVDDLVLKFAVLWVFTYVVAL-----FNLTLILLILALISLFSIPVIY 323
D 1482 -----FTFVNSVMSILAHNLEPINKQTFGG-----VIY 1509
QY 324 ERHQVQIDHYLGLANKSVK-----DAMAKIOAKIPGLK 356
D 1510 K-----NVGNVTVQOIGETIRPGDIVTFDKAKFSGQK 1540

RESULT 10
TI3286
cappuccino gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: TI3286
R:Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.
Genes Dev. 9, 2482-2494, 1995
A:Title: Cappuccino, a Drosophila maternal effect gene required for polarity of the egg
A:Reference number: Z17651; MUID:96033799; PMID:7590229
A:Accession: TI3286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1058 <EMM>
A:Cross-references: UNIPROT:Q24120; EMBL:U34258; NID:g1061333; PID:g1061334; PIDN:AAC4692
C:Genetics:
A:Gene: capu
A:Cross-references: FlyBase:FBgn0000256

Query Match 14.2%; Score 258.5; DB 2; Length 1058;
Best Local Similarity 16.2%; Pred. No. 2.1;
Matches 114; Conservative 51; Mismatches 103; Indels 435; Gaps 27;

QY 4 IDQSSLSV----- 11
D 340 LESASLASLGGAGVAGSLATATATTASSDNDQKTLQILKKRLNLCSTLAEVHAVVNELL 399
QY 12 SSTDSPPRP-----PAKYQF-----VTEPEDEEEDDEE----- 45
D 400 SSVDEPPRRPKRCVNLTELLNASEATVYENKTKGAECVKSFDTAETQETSEDCGCTK 459
QY 46 -----EDDEDLEELEVLERKPAAGLSAAVPPAAAPLLDFSSSDSVPPAP 90
D 460 CGQSTKVKSNKSAKEDGE-----KPHA---VAPPPPPPPPLPAFVAPPPPPPP 506
QY 91 RGPLP-----AAPPAAPERQPSWERSPAAPAS-----LPPAAAVLPK----- 129
D 507 PPPPPPLANYGAPPPPPPPPGSGSAPPPPPPPAPTEGGGGIPPPPPPMASPSKTTISPA 566
QY 130 -LPEDDE-----PP-----ARPPPPP-----AG 147
D 567 PLPDPAGNWFHRTNTRKMSAVNPPKPMRPLYWTRIVTSAPPAPPPSVANSTDSTENG 626
QY 148 ASPLAEP-----APPSTPAAPKRRGSGSVVDLLYWRDIKKT----- 185
D 627 SSPDEPPAANGADAPPTAPPATKE-----IWTETPLDNIDEFTLFSRQAI 675
QY 186 -----GVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217
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QY 229 IQAIQKDEGHP-----FRAYLESEVAISELVO----- 257
Db 777 IQINDKSQAAATLWDSLEEPHRTSEFEYLFSDTQOKKPLSEAVEKKNVKKI 836
QY 258 ----KYNSA-----LGHVNSTIKELRR-LFLVDDLDVSLKFAVLMVFTYVGFALFNGLTLL 309
Db 837 LLDGRSQTGVLISLSLHLEMDIQQAFTVDD----- 869
QY 310 ILALISLSIPVIYERHQVQIDHYLGLANKSVKDAWAKIQ----- 349
Db 870 --SVVDLETALAYE-----NRAQEDBLTKIRKYTYSKEEDLKLDKPEQF 914
QY 350 ----AKIPGLKRKA 359
Db 915 LHELAQIPNFAERA 928

RESULT 13
A59266
Unconventional myosin-15 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59266
R:Li, Y.; Wang, A.; Belyantseva, I. A.; Anderson, D. W.; Probst, F. J.; Barber, T. D.; Mil
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3530 <LTA>
A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:G6224682; PIDN:AAF05903.1; PID:G622
F:1225-1887/Domain: myosin motor domain homology <MMO>

Query Match 14.1%; Score 256.4; DB 2; Length 3530;
Best Local Similarity 10.1%; Pred. No. 48;
Matches 145; Conservative 54; Mismatches 124; Indels 1106; Gaps 37;

QY 17 PRPP-----PAFKQFV-----TEPEDEDEEE----- 40
Db 394 PPEVYFYFESASAFVYVWVPPPIPSPHNPYAHAMDDIAELEEDAGVERQGTSLP 453
QY 41 -----EEDDE 45
Db 454 SAAPEQQMDKPARSKSLIRKFLFRPQVKLFGEKLEVLPLPSLDIPLIGDADEE 513
QY 46 EDEDELEVL----- 57
Db 514 EDEELPPVSAVPGVGHFWGFLTPQRNLQALSAFGAHRGLGFGFGRPVPRPATSLA 573
QY 58 -----ERKPAAGL----- 65
Db 574 RFLKKTLEKKEIARLGRSQKTRAGGPAVREAAKYRFGYKLAGMDPEKGTPIVLRRAP 633
QY 66 ----- 65
Db 634 RARSSNDARRPPAPQAPRTLSHWSALLSPVPPRPPSSGPPAPPPLSPALSGLPRPASP 693
QY 66 -----SAAAVPPAAA----- 76
Db 694 YGSLRRHPPMAAPAHVPPAPQASGAWFVEPPAVSPVPPDLLAFPPGPRFGRSRRGA 753
QY 77 -----PLDFSSDSVPPAPR-----GPL--PAAPP 99
Db 754 AFGFGASPRARRRAWSPLASQPSLSRSSPGLGYCSPLAPSPQLSLRTGPFQPFPLFP 813
QY 100 A-----APERQ-----PSWERSPAAPAPSLPP-----AAAVLPSKL----- 130
Db 814 ARPRSLQESAPRAAGLPGPGSLPGSPRPPSPFPLGLCHSPRSSNLPLSRPLPHTWR 873
QY 131 -----PEDDE----- 135

Db 874 RLSEPPTRAVPQVRLPFRPRPRAGAWRAPLEHRESPREPDESETPTWTVPPLAPSDVDM 933
QY 136 --PPARPPPPPPAGA-----SPLAEPAP----- 157
Db 934 PPTQPPSPFWPGAGSRGSRFPVPENPFLLGLGVPSPPTLOPEDPAADMTRVFLGRH 993
QY 158 -----PSTPAAPK----- 165
Db 994 HEPGQQLTKSAGTPPEKPEBEENTLGDPLPAETKPTTPAPPKDVTPPKDITPPKDVLP 1053
QY 166 -----RR----- 167
Db 1054 QKTLRPSLSYPLAACDQTRATWPPHWRGTLPQAAAPLAPIRAPEPLPKGGERQAPGR 1113
QY 168 ----- 167
Db 1114 FAVVMPRVKLSFQFVGFPATLKQVQPIQDPKPRACSLRWSCMLWRADAYGMPVRVHT 1173
QY 168 -----GSGSS-----VVDLLYWRDI 182
Db 1174 PQSCHLGFGAACLSLGRSWEVGPSPWRKMHSTRNLSMRFRQHGEGDVEDMTQLEDL 1233
QY 183 KKTGVVFGASLFLLSLTVFSIVSVT-----AYIALALLSVT--ISFRIY----- 225
Db 1234 QBT-----TVLSNLKIRPERNLITYTVIGSILSVNPNYQMGFIVGPEQVQY 1279
QY 226 -----K 226
Db 1280 NGRALGENPPLFAVANLAFAMLDKAKQNCIIISGESGSKTEATKILIRLYAAMNQKR 1339
QY 227 GVIOAIQ-----KSDGHPFRAYLE-----SEVAISEELVOK-- 258
Db 1340 EVMQIKILEATPLLESFGNNAKTVRNDNSRFGKFEVLEFEGGVISGAIYSQYLLEKSRI 1399
QY 259 -----YNSA----- 263
Db 1400 VFQAKNERNYHIFVELLAGLPAQLRQAFSLQEAETYYLNOGNCIEIAGKSDADDFFRL 1459
QY 264 -----LGH----- 266
Db 1460 AAMEVLGFSDEQDSIFRILASILHGNVYFEKYTEDAQEASVVSAREIOQAVELLOIS 1519
QY 267 -----VNSTIKELRFL-----LVD--DLVDSLKFVLM--WVFTYVGL-- 302
Db 1520 PEGLKAITFKVTETRE--KIFTLTVESAVDARDAKLVYALLFSLITRVNALLVSP 1577
QY 303 -----FNGLTLLIL-----ALISLSIPVI-----YERHQVQ-- 329
Db 1578 RQDTLSIALDIYGFEDLSFNSFEQLCINANENLQYLFNKIVFOEQEYIREQIDWQE 1637
QY 330 ----- 329
Db 1638 ITFADNQRINLISLKPYGILRLDQCCFPQATDHTFLQKHYHGANPLYSKPMPLP 1697
QY 330 ---IDHYLGLA----- 337
Db 1698 EFTIKHYAGKTYQVHKFLDKNDQVRQDVLDFVRSSTRVVAHLFSSHAQAPQRLGK 1757
QY 338 -----NKSVDAMAKIQ-----AKIPGL 355
Db 1758 SSSVTRLYKAHTVAAKFOQSLLDLVERMERCNPLFMRLCKPNHKEPGL 1806

RESULT 14

S11515

formin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S11515

R:Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850-853, 1990

A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb deform

A:Reference number: S11515; MUID:90363291; PMID:2392150
A:Accession: S11515
A:Molecule type: mRNA
A:Residues: 1-1468 <WOY>
A:Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

Query Match 14.0%; Score 254.9; DB 2; Length 1468;
Best Local Similarity 14.5%; Pred. No. 6.3; Indels 103; Gaps 23;
Matches 97; Conservative 40; Mismatches 103; Indels 431; Gaps 23;

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QY 2 EDIDSSVSSSTGSPRP--PPA-----FKYQ----- 27
DQ 602 EEASEKGLGPEKITAPPQHQLPPIASEGFCDFNKEQTAKLPKNGGWWVGYRGP 661
QY 28 ---FVTEPEDEDEEE---EDEEDD----- 48
DQ 662 CPFLLEKEKTSRSELYLDLPDOSPTEQDDRTGRLQAVWPPPKTKDTEKVGKLYTE 721
QY 49 ---EDLEELEVLER----- 59
DQ 722 ABYQAAIHLKREKKEEITLQAFELKTFHIRGEHALVTARLEAEIENLKQOLEKRR 781
QY 60 -----KPAAGLSAAA----- 69
DQ 782 CEMRDVCISTDCCSPKAFRNVCIQDRETLKPCDAESKATRSQIVPKKLTISLTQL 841
QY 70 -----VPPAAAAPLLDFSSVPPAP-----R 91
DQ 842 SPSKSDKIHPFQTRGTSSSSQKISPPAPPPTPLPPL-----IPPPPLPPL 894
QY 92 GLPAAPPAAPRQSWERSPAAPAPSLPAAVLPKLPEDDEPPAPRPPPP----- 145
DQ 895 GLPPAPPPIPV-----CPVSPPPPPPPPP-----PTVPVPSDGGPPPPPPPLPNVLA 944
QY 146 ---AGASP-----LAEPAP-----PSTPAAPKRRGSGS 171
DQ 945 LPNSGGPPPPPPPPPPGLAPPGLSFGLSSSSSQVPRKPAIEPSCMPK----- 997
QY 172 SVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 231
DQ 998 ---LYWTR----- 1005
QY 232 IOKSDEGHP-----FRAYLSEVAISELVQ----- 257
DQ 1006 NDKSQDAAPTLDLSLEPHIRDTSFELYFSKDTTQKKKPLSEAYEKKNVKKIILKLD 1065
QY 258 -KYNSA---LGHVNSTIKELAR-LPLVDDLDVSLKFAVLMVFTVVGALFNGLTLLILA 312
DQ 1066 GRSQTVGLISLSLHLEMDIOQAFTVDD-----S 1096
QY 313 LISLFSIPVIYERHQVIDHYLGLANKSVKDAWKIQ----- 349
DQ 1097 VVDLETALAYE-----NRAQEDLTIRKYVETSKEEDLKLDPKQFLHE 1143
QY 350 -AKIFGLKKA 359
DQ 1144 LAQIPNFAERA 1154
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RESULT 15

T26998

Hypothetical protein Y48B6A.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26998

R:Wall, M.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20297

A:Accession: T26998

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-716 <WIL>

A:Cross-references: UNIPROT:Q9U2A6; EMBL:AL110490; NID:e1542263; PIDN:CAB54442.1; CESP:X

A:Experimental source: clone Y48B6A

C:Genetics:

A:Gene: CESP:Y48B6A.6

A:Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3

Query Match 14.0%; Score 254.7; DB 2; Length 716;

Best Local Similarity 16.9%; Pred. No. 1.1; Indels 353; Gaps 23;

Matches 101; Conservative 39; Mismatches 39; Indels 353; Gaps 23;

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QY 5 DOSSLVSSSTD-----SPRPP-----PAKYQFVTEPEDEDEDEEEDD 48
DQ 178 EMESLVQKQVDVLDQIMSSPPPPPTSPQLPPTPARITSVRSDESIEEERRRKESET 237
QY 49 EDLEELEV-----LEKPPAAGLSAAAAPPAAAPLLDFSDSDVPPAPRGP 95
DQ 238 ASFELEAEIMRISRP-----VPP-----PVL-----SIPPPPPNIPPLTPIQEVQSP 282
QY 96 -----AAPPAERQPSWE-----RSPAAAPAPSLP----- 121
DQ 283 PSPRTSVPPPIPPSPGSEDVNMDELIESFSDSVFNNSMSPPLPLPPLRESLETLEVT 342
QY 122 -----AAAVLPKLP-----DDEPPA----- 138
DQ 343 PEDPVTESKVEASPTPLPKATESLNESSIKALEGLEVKALEAQEASDDRPSAPTPIRDSS 402
QY 139 RPPPPPPAGAPLA-----EPAP-----PSTPAAPKRR 167
DQ 403 LPPPPPPKPTPLAIRRAGPIPTPOLLEMIHOEDCSIRPSSPTSVSHGSRQSPAPVKKP 462
QY 168 GSGSSVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 221
DQ 463 -----SVTVSPGLGLC 473
QY 222 -----FRIYKGVIAI- 232
DQ 474 DPNLSIEKPEEMKTEDTKPVETAPAPVDEALNDALDRNKINEATCLTKIPSLVKYF 533
QY 233 -----OKSDEGHP-----FRAYLSE----- 248
DQ 534 QNCSFDLNDKRSGENVPLKNNKISLYAESEFSESRKQIQYFSGIFKDYDEQDSYIDFN 593
QY 249 -----VAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLDVSLKFAVLM 293
DQ 594 ELKRNMEKLGAEQTHIAL-KELIKKVEDDQDKISQ-----REFLIIFRLAASGE----- 642
QY 294 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVIDHYLGLANKSVKDAWKIQAKI 352
DQ 643 -----LSCSEVFK--TLAESVDVSKGVGLGAN-----FTQAKI 674
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Search completed: June 23, 2005, 10:56:54

Job time : 32.9653 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:17:56 ; Search time 113.842 Seconds
(without alignments)
1619.338 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIQSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1732.7	95.0	1163	1 RTN4 RAT	Q9JK11 rattus norv
2	1721.6	94.4	356	2 Q8BH78	Q8BH78 mus musculus
3	1712.7	93.9	375	2 Q8BHF5	Q8BHF5 mus musculus
4	1711.5	93.9	357	2 Q8K3G7	Q8K3G7 mus musculus
5	1637	89.8	1162	2 Q8BGM9	Q8BGM9 mus musculus
6	1622.9	89.0	1163	2 Q8K3G8	Q8K3G8 mus musculus
7	1598.4	87.7	392	2 Q96B16	Q96B16 homo sapien
8	1518.4	83.3	1192	1 RTN4 HUMAN	Q9NQC3 homo sapien
9	1471.5	80.7	343	2 Q61PN0	Q61PN0 homo sapien
10	1012.1	55.5	986	2 Q81UA4	Q81UA4 homo sapien
11	1010.2	55.4	1046	2 Q8BGK7	Q8BGK7 mus musculus
12	992.2	54.4	578	2 Q8OW95	Q8OW95 mus musculus
13	988.7	54.2	639	2 Q8K290	Q8K290 mus musculus
14	960.5	52.7	658	2 Q6KSS8	Q6KSS8 gallus gall
15	914	50.1	199	1 RTN4 MOUSE	Q9P572 mus musculus
16	904	49.6	199	2 Q7YRW9	Q7YRW9 bos taurus
17	900	49.4	199	2 Q61M70	Q61M70 sus scrofa
18	899.1	49.3	315	2 Q61FY4	Q61FY4 xenopus tro
19	896	49.1	187	2 Q61G15	Q61G15 sus scrofa
20	895	49.1	199	2 Q7PCJ7	Q7PCJ7 macaca fasc
21	886.4	48.6	1024	2 Q6JRV2	Q6JRV2 xenopus lae
22	884.5	48.5	1043	2 Q6JRV0	Q6JRV0 xenopus lae
23	883.8	48.5	1032	2 Q6JRV7	Q6JRV7 xenopus lae
24	883.3	48.5	1055	2 Q6JRV1	Q6JRV1 xenopus lae
25	882.2	48.4	330	2 Q6JRV4	Q6JRV4 xenopus lae
26	880.8	48.3	1044	2 Q6JRV8	Q6JRV8 xenopus lae
27	880.5	48.3	311	2 Q6JRV3	Q6JRV3 xenopus lae
28	878.7	48.2	1013	2 Q6JRV9	Q6JRV9 xenopus lae
29	874.8	48.0	199	2 Q7T224	Q7T224 gallus gall
30	870.4	47.7	304	2 Q6JRW0	Q6JRW0 xenopus lae
31	870.3	47.7	323	2 Q6JRW1	Q6JRW1 xenopus lae

32	861.2	47.2	316	2 Q6JRW2	Q6JRW2 xenopus lae
33	855.6	46.9	720	2 Q7TNB7	Q7TNB7 mus musculus
34	844	46.3	179	2 Q9GM33	Q9GM33 macaca fasc
35	826.3	45.3	776	1 RTN1 HUMAN	Q16799 homo sapien
36	826.2	45.3	780	2 Q8K0T0	Q8K0T0 mus musculus
37	823.2	45.2	780	2 Q8K4S4	Q8K4S4 mus musculus
38	807.4	44.3	777	1 RTN1 RAT	Q64548 rattus norv
39	793.9	43.5	760	2 Q90638	Q90638 gallus gall
40	773	42.4	193	2 Q61FY5	Q61FY5 xenopus tro
41	766.1	42.0	199	2 Q6PB23	Q6PB23 xenopus lae
42	761	41.7	193	2 Q6JRV6	Q6JRV6 xenopus lae
43	746.1	40.9	199	2 Q6JRW3	Q6JRW3 xenopus lae
44	744	40.8	193	2 Q6JRW4	Q6JRW4 xenopus lae
45	736.6	40.4	214	2 Q7T222	Q7T222 carassius a

ALIGNMENTS

RESULT 1			
RTN4 RAT			
ID	RTN4 RAT	STANDARD;	PRT; 1163 AA.
AC	Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DE	Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)		
DE	(Glut4 vesicle 20 kDa protein).		
GN	Name=Rtn4; Synonyms=Nogo;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=Adipocyte;		
RX	MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;		
RA	Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.B.;		
RT	"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";		
RL	Biochim. Biophys. Acta 1450:68-76(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).		
RX	MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;		
RA	Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,		
RA	Spillmann A.A., Christ F., Schwab M.E.;		
RT	"Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1.";		
RL	Nature 403:434-439(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).		
RC	STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;		
RA	Ito T., Schwartz S.M.;		
RT	"Cloning of a member of the reticulon gene family in rat: one of two minor splice variants.";		
RL	Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	FUNCTION.		
RX	MEDLINE=20033691; PubMed=12037567; DOI=10.1038/417547a;		
RA	GrandPre T., Li S., Strittmatter S.M.;		
RT	"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";		
RL	Nature 417:547-551(2002).		
CC	-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By similarity).		
CC	-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By similarity).		
CC	-!- SIMILARITY:		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=4;		
CC	Name=1; Synonyms=Nogo-A, NI-220-250;		

Db	537	CESELNEATGT	KIAYETKVDLVQTSSEAIQESIIYPTAQLCPSEAEATPSPVLPIVMEA	596
Qy	172	-	-	171
Db	597	PLNSLLPSTGASVAQSASP	LEVPSPVSVDGIKLEPENPPPYEAMSVALKTSKSKEIK	656
Qy	172	-	-	171
Db	657	EPESFNAAQAEEAPYISIA	CADLIKETKLSTEPSPEFSNYSIAKFEKSPDHCHLVDSDS	716
Qy	172	-	-	171
Db	717	SPESEPVDFSDSDSIP	EVPQTQEAVMLMKSLTEVSETVTQHKKERLSASPOEVGKPY	776
Qy	172	-	-	171
Db	777	LESFQPNLHITKDAASNEI	PTLTKETISIQMEEFNTAIYNSDDLLSSKEDKMKESETPS	836
Qy	172	-	-	171
Db	837	DSSPIIIDEPFTFVSAKD	DSPKYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNT	896
Qy	172	-	-	171
Db	897	YPKDEAHVSDSFSGSRSS	VSKVPDLLPNVSALESQIEMGNIVKPVLTKBAEKLPDSTE	956
Qy	172	-	-	171
Db	957	KEDRSITAVLSAELNKTS	VDLLYWRDIKTGVFGASFLLLSLTFSIVSYTAYIALA	1016
Qy	215	LLSVTISFRYKGVIOAQK	SDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL	274
Db	1017	LLSVTISFRYKGVIOAQK	SDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEL	1076
Qy	275	RRLFLVDDLVDLSKF	FAVLMWTFYTGALFNGLTLLILALISLFSIPVIYERHQVIDHYL	334
Db	1077	RRLFLVDDLVDLSKF	FAVLMWTFYTGALFNGLTLLILALISLFSIPVIYERHQVIDHYL	1136
Qy	335	GLANKSVKDAMAKIOAKI	PGLKRKAD 360	
Db	1137	GLANKSVKDAMAKIOAKI	PGLKRKAE 1162	
RESULT 6				
ID	Q8K3G8	PRELIMINARY;	PRT; 1163 AA.	
AC	Q8K3G8;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Nogo-A.			
GN	Name=Rtn4;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RA	Jin W., Long M., Li R., Ju G.;			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AV114152; AAM77068.1; -.			
DR	MGD; MGI:1915835; Rtn4.			
DR	GO; GO:0005783; C-endoplasmic reticulum; IEA.			
DR	InterPro; IPR003388; Reticulon.			
DR	Pfam; PF02453; Reticulon; 1.			
DR	PROSITE; PS50845; RETICULON; 1.			
SQ	SEQUENCE 1163 AA; 126690 MW; 6BSF362799417EA4 CRC64;			
Query Match 89.0%; Score 1622.9; DB 2; Length 1163;				
Best Local Similarity 29.7%; Pred. No. 4.7e-44;				
Matches 347; Conservative 2; Mismatches 7; Indels 811; Gaps 5;				

RN [5] SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RP TISSUE=Placenta, and Skeletal muscle;
 RC Ito T., Schwartz S.M.;
 RA "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RL "Isolation of a cell death-inducing gene.";
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Embryonic;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RL "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.P., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RL "Novel human cDNA clones with function of inhibiting cancer cell
 growth.";
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RL "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Jordan H., Karsan A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RL "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Umbilical cord blood;
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RL "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
 RA GrandPré T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RL "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
 RA Fournier A.E., Grandpré T., Strittmatter S.M.;
 RL "Identification of a receptor mediating Nogo-66 inhibition of axonal
 RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RC MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;
 RA Ng C.E.L., Tang B.L.;
 RL "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ251383; CAB99248.1; -;
 CC EMBL; AJ251384; CAB99249.1; -;
 CC EMBL; AJ251385; CAB99250.1; -;
 CC EMBL; AB040462; BAB18927.1; -;
 DR
 DR
 DR


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Q8BGK7
ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
AC Q8BGK7;
DT 01-WAR-2003 (TREMELrel. 23, Created)
DT 01-JUN-2003 (TREMELrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE RTN4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvCj7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RL human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvCj7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102280; AAM73502.1; -
DR EMBL; AY102286; AAM73507.1; -
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 55.4%; Score 1010.2; DB 2; Length 1046;
Best Local Similarity 29.2%; Pred. No. 4.3e-24;
Matches 249; Conservative 25; Mismatches 80; Indels 498; Gaps 14;

QY 5 DOSSLVSSSTDSPPPPPA-----PKYQVTPPEDE----- 35
DB 197 DKEDLVCSAALHPQESPATLTKVVKEDGWSPEKTMDFNEMKMSVVPVREYADFEP 256
QY 36 -----EDEEEDEEDED----- 50
DB 257 FEQANEVKDITYGSRDVLAAANMESKVDKCFEDSLQKGGKQSESNENASFPRTPE 316
QY 51 -----LEELEVLERKPAAGLSAAAVPP 72
DB 317 LVKDGSRVITCDSPSSATESTAAINFVLEDHTSENKTDKKIEBK--AQIITEKSP 374
QY 73 AAAAPLLDFSSDS-----VPPAPRGPLPAAPPAERQ----- 105
DB 375 KTSNPFLVAIHDSADYVTDNLKVTAEVATMPEGLTDLVQACSELSNEATGTGKIA 434
QY 106 -----PSWERSPAAPAPSLP-----PAAAVLPSPKLPEDD 134
DB 435 YETKVDLVQTSIAQESYPTAQLCPSEAEATPSVLPDVMAPLNSLLPSTGASVA 494
QY 135 EP-----PARPPP----- 142
DB 495 QPSASPLEVPSPVSDGKLEPENPPVEEAMSVALKTSDSKEEIKEPESFNAAQAEAA 554
QY 143 -----PPPA-----GASPLAEP-----A 156
DB 555 PYISIACDLIKETKLSPEFSFSNYSEIAKPEKSVDPCHCELVDDSSPESEPVDFLSDS 614

QY 157 PPSTP-----AAPKRG----- 168
DB 615 IPEVPQTOEEAVMLMKESLITEVSETVTOHKKERLSASPOEVGKPYLESFQPNLHITKDA 674
QY 169 ----- 168
DB 675 ASNEIPTLTKKETISLQMEEFNTAYSNDLLSSKEDKMKESETPSDSSPIEIIDEFPTF 734
QY 169 -----SG----- 170
DB 735 VSAKDDSPKEYTDLEVSNNKSEIANVQSGANSLPCSELPCLSFKNTPKDEAHVSDEFSK 794
QY 171 ----- 170
DB 795 SRSSSVKVPLLLPNVSALESQIEMGNIYKPKVLKEAEKLPDSTEKEDRSITAVLSAEL 854
QY 171 --SSVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGV 228
DB 855 NKTSVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALLSVTISFRIYKGV 914
QY 229 IOATOKSDEGHPPFRAYLSEVAISEELVOKYSNSALCHVNSTIKELRRLFLVDDLDVSLK 288
DB 915 IOATOKSDEGHPPFRAYLSEVAISEELVOKYSNSALCHVNSTIKELRRLFLVDDLDVSLK 974
QY 289 FAVLMWVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 348
DB 975 FAVLMWVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 1034
QY 349 QAKIPGLKPKAD 360
DB 1035 QAKIPGLKPKAB 1046

RESULT 12
Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON TER 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171B4AC61 CRC64;

Query Match 54.4%; Score 992.2; DB 2; Length 578;
Best Local Similarity 42.4%; Pred. No. 4.1e-24;
Matches 233; Conservative 13; Mismatches 79; Indels 225; Gaps 8;

QY 17 PPRPPP---AFKYQVTPPEDEDEEDEDDE-----DLEELEVLERKPA 63
DB 48 PENPPPEEAMSVALKTSDAKEEIKEPESFNAAQAEAPYISIACDLIKETKLSPEP 107
QY 64 GLS-----AAAVP-----PAAAPLLDFSSDSVPPAPR----- 91
DB 108 GFSNYSIEAKPEKSVDPCHCELVDDSSPESEPVDFLSDSIEFVPTQEEAVMLKESL 167
QY 92 -----GPLPAAPPAERQ----- 106
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Db 168 VSETVQHKKHERLSASPOEVGKPYLESFQPNLHITKDAASNEIPTLTCKTETISLQMEEF 227
QY 107 -----
Db 228 NTAIYSNDLLSSKEDKMEKETSFSDSPIETIDFPFTFVSADKDSPEKTYTDLEVSNKSE 287
QY 107 -----
Db 288 IANVSGANSPLCSSELPDLSFKNTYPKDEAHVDSFESKRSVFKVPLLLPNVSALESQ 347
QY 129 -----
Db 348 IEMGNIVKPKVLTKEAEKLPSTEDR-----SLTAVLSAELNK 388
QY 171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLSVTISPRIYKGVITQ 230
Db 389 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLSVTISPRIYKGVITQ 448
QY 231 ALOKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPA 290
Db 449 ALOKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPA 508
QY 291 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAKIAQ 350
Db 509 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAKIAQ 568
QY 351 KIPGLKRXAD 360
Db 569 KIPGLKRXAE 578
RESULT 13
ID Q8K290 PRELIMINARY; PRT; 639 AA.
AC Q8K290;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC032192; AAH32192.1; -.
DR MGI; 1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 639 AA, 70312 MW, 309A19DA37603F11 CRC64;
Query Match 54.2%; Score 988.7; DB 2; Length 639;
Best Local Similarity 42.2%; Pred. No. 6.8e-24;
Matches 232; Conservative 14; Mismatches 79; Indels 225; Gaps 8;
QY 17 PRPPP---AFKYPVTEPEDEDEDEDEDEDEDE-----DLEELVLERKPA 63
Db 109 PENPPPYEAMSVALKTSDAKEEIKPESEFNAAQAEAPYISICDLIKETKLTSTPEP 168
QY 64 GLS-----AAAVP-----PAAAPLLDFSSDSVPPAPR----- 91
Db 169 EFSNYSETAKESVPDHCVELVDDSSPESEPVDFSDSDSIPEVPQTQBEAVMLKESL 228
QY 92 -----GPLPAAPPAPERQ----- 106
Db 229 VSETVQHKKHERLSASPOEVGKPYLESFQPNLHITKDAASNEIPTLTCKTETISL 288
QY 107 ----- 106
Db 289 NTAIYSNDLLSSKEDKMEKETSFSDSPIETIDFPFTFVSADKDSPEKTYTDLEV 348
QY 107 -----SWERSPAAPAPSLPAAAVLPS- 128
Db 349 IANVSGANSPLCSSELPDLSFKNTYPKDEAHVDSFESKRSVFKVPLLLPNVSALES 408
QY 129 -----KLPEDDEPPAPPPPPPPAGASPLAEPAPSTPAAPKRRGSG 170
Db 409 IEMGNIVKPKVLTKEAEKLPSTEDR-----SLTAVLSAELNK 449
QY 171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLSVTISPRIYKGV 230
Db 450 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALLSVTISPRIYKGV 509
QY 231 ALOKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLK 290
Db 510 ALOKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLK 569
QY 291 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAKIA 350
Db 570 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAKIA 629
QY 351 KIPGLKRXAD 360
Db 630 KIPGLKRXAE 639
RESULT 14
ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name=NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
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DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;
Query Match 52.7%; Score 960.5; DB 2; Length 658;
Best Local Similarity 35.5%; Pred. No. 6.1e-23;
Matches 229; Conservative 41; Mismatches 70; Indels 305; Gaps 16;
QY 3 DLDQSS-----LVSSSTSPPPPPAP----- 24
Db 32 DLVOTSESQETLKPVTLQPCSFEDSEAPSPVLPDIVMEAPLSSTGAGAEASTVQLETS 91
QY 25 -----KYQFV-----TEPED--- 34
Db 92 QLGTFVTTSYENYKKEAKPPLYQEAVMNPLTQQAKEEUTLKKADRESSTSPEDLET 151
QY 35 ----- 34
Db 152 PYISACDLIKETKVGESASPLTDYSTPTITEHLSDQVSEHKELAEKLSQFGKCDLF 211
QY 35 -----EDEEE-----EDEED-----DEDEELE 55
Db 212 SRQVMPDFPGKESEDQTLTLNGKSVENIETDEQERLVDSLAAATGKPYLESFQDELDSSK 271
QY 56 VLKPKAAGLSAAVPPAAAPL-----LDSSD---SVPPAP---RGPLPAAPPAAP 102
Db 272 IYVTPQSEP-TPAKTAKAEKIPLOMEELNALAYSTDVSVAMPKPGDGSLSPSPSVVE 330
QY 103 E-----RQPSWERSPAAPAPSLP--- 120
Db 331 DDFVMLVDPKTGTEFVAEVTDRVTHKNESKDISEIRDEKQ-----APLTLPD 382
QY 121 -----PAAVLP SKL-----PEDE 135
Db 383 LSVRNVEVKTEDDAHALKSKLQADREVPEVSMVSLPATGTSPSSTEKEIVSVGPEAFE 442
QY 136 PPARPPPPPPAGASPLAEPAPSTPAAPKPRGSGSVVDLLYWRDIKKTGVVFGASLFL 195
Db 443 KEAE-----RGAASAKEKETAVFSA---KLVSSVVVDLLYWRDIKKTGVVFGASLFL 493
QY 196 LLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEEL 255
Db 494 LLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESDVAVSEEL 553
QY 256 VQKYSNSALCHVNSTIKELRLFLVDLLVDSLKFAVLMMVFTYVGCALFNGLTLILLALIS 315
Db 554 IQKYSVVLGHNGTGVKELRLFLVDLLVDSLKFAVLMMVFTYVGCALFNGLTLILLALIS 613
QY 316 LFSIPVYERHQQVDHYLGLANKSVKQAMAKIQAKIPLGRKAD 360
Db 614 LFSVPVYERHQQVDHYLGLVKNVKNVQAMAKIQAKIPLGRKTE 658
RESULT 15
RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99F72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN Name=Rtn4; Synonyms=Nogo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C.; Craggs P.D.; Morris N.J.;
RT "Mouse vp20/RTN4C cDNA.";
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Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE OF 170-199 FROM N.A.

STRAIN=C57BL/6J; TISSUE=Embryo;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Gojibori T., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

Nature 420:563-573 (2002).

-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help block the regeneration of the nervous central system in adults (By similarity).

-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=1;

Comment=A number of isoforms may be produced;

Name=1;

isoform=Q99P72-1; Sequence=Displayed;

-!- SIMILARITY: Contains 1 reticulon domain.

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EMBL; AF326337; AAK08076.1; --;

EMBL; AK003859; --; NOT ANNOTATED_CDS.

MGI; MGI:1915835; Rtn4.

GO; GO:0005783; C:endoplasmic reticulum; IDA.

GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.

GO; GO:0005635; C:nuclear membrane; ISS.

GO; GO:0005515; F:protein binding; ISS.

GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.

GO; GO:0030517; P:negative regulation of axon extension; ISS.

GO; GO:0007399; P:neurogenesis; IDA.

InterPro; IPR003388; Reticulon.

Pfam; PF02453; Reticulon; 1.

PROSITE; PS50845; RETICULON; 1.

Alternative splicing; Endoplasmic reticulum; Transmembrane.

DOMAIN 1 25 Cyttoplasmic (Potential).

TRANSMEM 26 50 Potential.

```
FT DOMAIN      51 137 Lumenal (Potential).
FT TRANSMEM   138 162 Potential.
FT DOMAIN     163 199 Cytoplasmic (Potential).
FT DOMAIN      12 199 Reticulon.
SQ SEQUENCE   199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match      50.1%; Score 914; DB 1; Length 199;
Best Local Similarity 83.3%; Pred. No. 1.2e-22;
Matches 190; Conservative 3; Mismatches 5; Indels 30; Gaps 2;

QY 133 DDEPPARPPPPAGASPLAEPAPPSTPAAPKRRGSGSVVDLLYWRDIKKTGVVFGAS 192
Db 2 DDQ-----KRWK-DKVVDDLLYWRDIKKTGVVFGAS 31

QY 193 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPPRAYLESEVAIS 252
Db 32 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPPRAYLESEVAIS 91

QY 253 BELVOKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLMVFTYVVGALFNGLTLLILA 312
Db 92 BELVOKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLMVFTYVVGALFNGLTLLILA 151

QY 313 LISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQAKIPGLKRRAD 360
Db 152 LISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQAKIPGLKRRAE 199
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Search completed: June 23, 2005, 10:55:54
Job time : 118.842 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 09:47:53 ; Search time 30.5423 Seconds
(without alignments)
882.327 Million cell updates/sec

Title: US-09-830-972-29-FUSED

Perfect score: 1850

Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIOAKIPLKRAE 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927	50.1	199	2	US-08-700-607-1
2	927	50.1	201	4	US-09-949-016-9124
3	827.7	44.7	776	2	US-08-700-607-5
4	827.7	44.7	776	4	US-09-949-016-6998
5	804.9	43.5	439	4	US-09-949-016-9180
6	789.8	42.7	356	2	US-08-700-607-6
7	684.2	37.0	208	2	US-08-700-607-7
8	666	36.0	267	2	US-08-700-607-8
9	627.9	33.9	192	4	US-09-949-016-8859
10	599.1	32.4	588	4	US-09-949-016-7290
11	541.9	29.3	168	4	US-09-149-476-563
12	538.3	29.1	241	2	US-08-700-607-3
13	518	28.0	219	4	US-09-270-767-45132
14	348.9	18.9	75	4	US-09-621-976-4600
15	348.9	18.9	75	4	US-09-621-976-4601
16	347	18.8	68	4	US-09-513-999C-6304
17	285	15.4	92	4	US-09-149-476-411
18	276.2	14.9	1027	4	US-09-902-540-11750
19	259.7	14.0	1248	2	US-09-080-897-2
20	259.7	14.0	1248	3	US-09-323-735-2
21	258.2	14.0	1315	3	US-08-899-595-3
22	256.5	13.9	1255	2	US-09-080-897-4
23	256.5	13.9	1255	3	US-08-899-595-1
24	256.5	13.9	1255	3	US-09-323-735-4
25	248.2	13.4	114	4	US-09-513-999C-7861
26	247	13.4	2090	4	US-09-538-092-1081
27	247	13.4	2120	4	US-09-949-016-9768

28	246.1	13.3	8991	4	US-08-714-741-32	Sequence 32, Appl
29	245.8	13.3	1070	3	US-08-922-635-22	Sequence 22, Appl
30	245.8	13.3	1504	4	US-09-364-206-2	Sequence 2, Appl
31	244.5	13.2	990	4	US-09-949-016-10562	Sequence 10562, A
32	243.6	13.2	1719	2	US-08-459-568-4	Sequence 4, Appl
33	243.6	13.2	1719	2	US-08-399-411-4	Sequence 4, Appl
34	243.6	13.2	1719	3	US-08-516-859A-4	Sequence 4, Appl
35	243.6	13.2	1719	3	US-09-586-472-4	Sequence 4, Appl
36	243.6	13.2	1719	4	US-09-528-706-4	Sequence 4, Appl
37	241.5	13.1	933	3	US-08-764-870-14	Sequence 14, Appl
38	241.5	13.1	933	3	US-08-980-115-14	Sequence 14, Appl
39	238.7	12.9	1540	4	US-09-949-016-11382	Sequence 11382, A
40	238.7	12.9	1540	4	US-09-949-016-11383	Sequence 11383, A
41	238.7	12.9	1706	2	US-08-459-568-2	Sequence 2, Appl
42	238.7	12.9	1706	2	US-08-399-411-2	Sequence 2, Appl
43	238.7	12.9	1706	3	US-08-516-859A-2	Sequence 2, Appl
44	238.7	12.9	1706	3	US-09-586-472-2	Sequence 2, Appl
45	238.7	12.9	1706	4	US-09-528-706-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hallman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Consensus
; US-08-700-607-1

Query Match 50.1%; Score 927; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.1e-33;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 233

Db 12 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 234 QKSDGHPHPRAYLESEVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 293
Db 72 QKSDGHPHPRAYLESEVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 131
QY 294 MVVFTYVGFALFNGLTLLIALLSLFSVPVIYERHQAQIDHYLGLANKNVKDAWAKIOAKI 353
Db 132 MVVFTYVGFALFNGLTLLIALLSLFSVPVIYERHQAQIDHYLGLANKNVKDAWAKIOAKI 191
QY 354 PGLKRAE 361
Db 192 PGLKRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 50.1%; Score 927; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 233
Db 14 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 234 QKSDGHPHPRAYLESEVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 293
Db 74 QKSDGHPHPRAYLESEVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 133
QY 294 MVVFTYVGFALFNGLTLLIALLSLFSVPVIYERHQAQIDHYLGLANKNVKDAWAKIOAKI 353
Db 134 MVVFTYVGFALFNGLTLLIALLSLFSVPVIYERHQAQIDHYLGLANKNVKDAWAKIOAKI 193
QY 354 PGLKRAE 361
Db 194 PGLKRAE 201

RESULT 3
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5
Query Match 44.7%; Score 827.7; DB 2; Length 776;
Best Local Similarity 27.1%; Pred. No. 3.6e-28;
Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;
QY 6 QSP-----
Db 70 OSPVAMETASTAGVAGVSSAMDHFTSTSKDGBGCVTSLSDICYPPQEDSTYFTGILOK 129
QY 10 ----VSSSDSPR---POP-----
Db 130 ENGHVTISEFEELTGPSPIDVPGIERSGLFSSDSGIEMTPAESTEVNKILADPLDQM 189
QY 22 ---AFKYQVREPEDEEEEEDEDEDELE-----
Db 190 KAEAVKYIDITRPEVKHQEQHPELKDLDKFKNDYDISIKPGVREPKPAPVEGKI 249
QY 51 -----ELE-----
Db 250 IKDHLLBESTFAPYIDDLISEBORRAPQITTPVKITLTIEPVSVETTTOBKTPEKODICUK 309
QY 54 -----
Db 310 PSPDVTPTVTYVSEPEDDSFGSITPPSSGTEPSAESQKSGSISEDELITAIKEAGLSYE 369
QY 65 ----AAPV-----PTAPAGAPL-----
Db 370 TAENPRPVQLADRPVKARSGPPTIP---SPLDHEASSAESGDSIEILVSEDPMAEDA 426
QY 79 -----MDQNDVFPAPRGPPLPAAAPV-----APE 103
Db 427 LPSGYVSGHVGPP-----PSPASPSIQSYILREREAELDSIELIESCDASASEESPK 482
QY 104 RO---PSWDPSVS-----STVPAPSPLSAAAVSP 130
Db 483 REQDSPPMKPSALDAIRETGVRAEERAPSRGLAEPGSFLDYPSTEPQGP-----534
QY 131 SKLPED-----EPPARPPPPPPASVQAEVWTPAP-APAAP-----STSVVDLL 178
Db 535 -ELPPGDGALEPETMPLPRKPEEDSSNQSPAATKPGPGFGAPPPLFLNKKOKAIDLL 593

Db 247 LNKQKXIDLLYWRDIKQGIYVGFSGFLLLSLTFQSVSVVAYLALAAALSATISFRIYKS 306
QY 229 VTQAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCIYKELRRLFLVDDLVDLSL 288
Db 307 VLQAVQKTDGHPFRAYLEITLSQEQIKYKTDCLQFYVNSTLKLRLFLVQDLVDLSL 366
QY 289 KEAVLMMVTVYVGNLFGNLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKVNDKAMAK 348
Db 367 KEAVLMMVTVYVGNLFGNLTLLMAVSMFTLPVVYVYVHQAIQIDYLGVLVRTHINAVAK 426
QY 349 IQAKIPGLKRAE 361
Db 427 IQAKIPGAKRAE 439

RESULT 6
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
US-08-700-607-6

Query Match 42.7%; Score 789.8; DB 2; Length 356;
Best Local Similarity 42.6%; Pred. No. 3.9e-27;
Matches 169; Conservative 42; Mismatches 74; Indels 112; Gaps 10;
QY 16 PPRP-QPAPFYQVREPDEE-----EEEEEEEEDEDELEEVLERK 58
Db 21 PPSPASPSIQYSLRREAREALDSLIIESCDASSASESPKREQD----- 66
QY 59 PAAGLSAAPVTPAPAGAPLMFGNDFVPPAPRGPLPAAPPVAP-----E 103
Db 67 -----SPPMKPSALDAIREETGVRAEE 88

QY 104 ROPS-----WDPS---PVSVTPAPSPLSAAVSPSKLPEDD-----EPPARPPPPPPASV 151
Db 89 RAPSRRLAEPGSGFDYDSTEPQPGP-----ELPPDGALEPETPMLPRKPEEDSS 139
QY 152 SPQAEFVWTPPAP-APAAP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 204
Db 140 SNQSPAATKPGPLGPGAPPLFLNKKQKAIIDLLYWRDIKQTGIVFGSFLLLLSLTQFS 199
QY 205 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISELVQKYSNSA 264
Db 200 VVSVVAYLALAAALSATISFRIYKSVLQAVQKTDGHPFRAYLEITLSQEQIKYKTDCL 259
QY 265 LGHVNCTIKELRRLFLVDDLVDLSLKFVLMVWTVYVGNLFGNLTLLILALISLFSVPVIY 324
Db 260 QFYVNSTLKLRLFLVQDLVDLSLKFVLMVWTVYVGNLFGNLTLLMAVSMFTLPVY 319
QY 325 ERHQAIQIDHYLGLANKVNDKAMAKIQAKIPGLKRAE 361
Db 320 VKHQAIQIDYLGVLVRTHINAVVAKIQAKIPGAKRAE 356

RESULT 7
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307311
US-08-700-607-7

Query Match 37.0%; Score 684.2; DB 2; Length 208;
Best Local Similarity 62.4%; Pred. No. 6.7e-23;
Matches 131; Conservative 35; Mismatches 36; Indels 8; Gaps 1;
QY 152 SPQAEFVWTPPAPAPAPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSVTAY 211
Db 7 STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAY 58


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; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match          32.4%; Score 599.1; DB 4; Length 588;
Best Local Similarity 26.9%; Pred. No. 2.8e-18;
Matches 157; Conservative 56; Mismatches 122; Indels 249; Gaps 18;

QY 14 DSDPRQ-----PAFKYQFVRE-----PEDEE----- 35
   |||:
Db 18 DERPRACGTAGVGGPDAGRGAMQVLFVAH--CKEAPSTASSTPDTSTEGNDSD 75
   |||:
QY 36 -----EEEEEEED----- 46
   |||:
Db 76 DPRELHAREFSEDEEEETSDWGTTPRELTSYIADFVGVGSGRRDSTARPRPQRS 135
   |||:
QY 47 -----EDLELEVLERKPAAGLSAAPVPTAPAGAPLMD--FGNDFVPPAP 90
   |||:
Db 136 VSEPRDHPQPSLGDSLESIPLSQSPFERRGDP-DTAPPSEPFLEDLRLDLHLGWVA 194
   |||:
QY 91 RG-----PLPAAPPVAPER-----QPSWDP-----SPV 113
   |||:
Db 195 RTGSGEDSSTSSSTPLEDEEPOEPNRLETGEAGEBOLDLRLRLAOPS-SPEVLTPQLSPG 253
   |||:
QY 114 SSTVPAPSLAANVSPSKLPEDDEPPAP----- 143
   |||:
Db 254 SGTPOAGTP-----SPSRSDNSGPEEPFLLEEKONGKPLERPFVRGQCCLDSTDQLRF 307
   |||:
QY 144 -----PPPPASVSPQAEPPVW-----TPP----- 162
   |||:
Db 308 TVEPRLLGTAMWLKTSLLANVKTVPLELSP---PLMTATGWQVGRPTPTPVLRLVLL 364
   |||:
QY 163 -----APAPAAPSTS-----VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVA 210
   |||:
Db 365 KWAKSPRSRGVPSLSLGDWMSKADLLYWKDTRTSGVFTGLWVSLCLLHFSIVSVA 424
   |||:
QY 211 YIALALLSVTFRIYKGVIOAKQKDEGHPRFAVLESEVAISEELVQKYSNLSALGVNC 270
   |||:
Db 425 HLALLLCCTISLRVYKRVQLAVHRGDGANPFQAYLDVDTLTRQTERLSHQITSRVVS 484
   |||:
QY 271 TIKELRRLVDDVLSLKFVLMVFTVVGALFNLGLTLLIALLSLFSVPVIVYERHQAO 330
   |||:
Db 485 AATQLRHFLVEDVLSLKLALLFYLTFTVGAIFNLGLTLLIILGVGLFTPIPLLYRQHQAO 544
   |||:
QY 331 IDHYGLANKNVKDMAKIQAIPGL-----KKRAE 361
   |||:
Db 545 IDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAAAAVSGSKAKAE 588

RESULT 11
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
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EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 29.3%; Score 541.9; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 8.9e-17;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

QY 196 LLSLTVFSIVSVTAYIALLSVTISPRIYKGVIOAQKSDGHPFRAYLSEVAISSE 255
Db 1 MLLSLAASFVSVSVSILILLSVTISPRIYKSVIOAQKSEGHPPFRAYLDVDTLSSE 60
QY 256 LVQKYSNSALGHVNCTIKELRRLFLVDLVDLSKFAVLMMVFTYYGALFNGLTLLTLLALI 315
Db 61 AFHNTYMAVHINEALKLIIRLFVEDLVDLSKLAFLVFWLMTYYGAVENGITLLILAE 120
QY 316 SLFSPVVIYERHQADIDHYLGLANKVNDMAKIOAKIPGL-KRKAE 361
Db 121 LIFSVPVIYERYKTDIDHYVGIARDQTKSIVEKIOAKLPGIARKKAE 167

RESULT 12
US-08-700-607-3
Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

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ALIGNMENTS


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QY 172 ----- 171
Db 421 DKCFADSLQTNHKESSNDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTSENKTDKKEIEKKAQIVTEKNTSTKSNPFLVAAQDSETDVTTDNLTKYTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTPDLVQEAACESLNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSE 600
QY 172 ----- 171
Db 601 ESEATPSPVLPDI VMEAPLNSAVPSAGASVIQSPSSPLEASSVNYSEIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKEEIKPENINAAQTEAPYISACDLIKETHKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSSPDSEPVDFSDDSIPDVPOKQDETVMVKESLTETSPESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKBAQIRETETFSDSPIEIDEFFTLISSKTSKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQPKVEKISFSDPSKNGSATSKVLLPPDVLSALAT 960
QY 172 ----- 171
Db 961 QAEIESIVKPVLVKAEKLPDTEKEDRSFSAELSSTSVVLDLYWRDIKKTGV 1020
QY 190 FGASLFLLSLVFVSIVSVTAYIALALLSVTISFRYKGVIOAIQKSDGHPFRAYLESE 249
Db 1021 FGASLFLLSLVFVSIVSVTAYIALALLSVTISFRYKGVIOAIQKSDGHPFRAYLESE 1080
QY 250 VAISELVQYNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGTL 309
Db 1081 VAISELVQYNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALFNGTL 1140
QY 310 LIALISLFSVPVIERHQAQIDHYGLGANKNVKDMAKIOAKIPGLKRAE 361
Db 1141 LIALISLFSVPVIERHQAQIDHYGLGANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 11
US-09-830-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, Irun R.
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; FILE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23
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Query Match 95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEELVLERKPA 60
Db 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEELVLERKPA 60
QY 61 AGLSAAPVPTAPAGAPLMDFGNDVPPAPRGPLPAAPVAPERQPSWDPPSVSTVPAP 120
Db 61 AGLSAAPVPTAPAGAPLMDFGNDVPPAPRGPLPAAPVAPERQPSWDPPSVSTVPAP 120
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEVMTTPPAPAPAAPPS 171
Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEVMTTPPAPAPAAPPS 180
QY 172 ----- 171
Db 181 SSGSVDETALFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPVLETAASLP 240
QY 172 ----- 171
Db 241 LSAASFKEHYGLNLSVLTPTGTLQENVSEASKEVSEKATLLIDRLDTFSELEYSEM 300
QY 172 ----- 171
Db 301 GSSFSVSPKAESAVIVANPREIIVKNKDEBEKLVNNILHNQQLPTALTAKLVEDEVV 360
QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFRVMEVKDSKEDSMDLAAGKIESNLSKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHKESSNDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTSENKTDKKEIEKKAQIVTEKNTSTKSNPFLVAAQDSETDVTTDNLTKYTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTPDLVQEAACESLNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSE 600
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Db 601 ESEATPSPVLPDI VMEAPLNSAVPSAGASVIQSPSSPLEASSVNYSEIKHEPENPPYE 660
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Db 721 MAKVEQVPDHSSELVEDSSPDSEPVDFSDDSIPDVPOKQDETVMVKESLTETSPESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
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; APPLICANT: Jiang, Yudiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71

Query Match      95.0%; Score 1756.9; DB 14; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

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Db      1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60

Qy      61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQSPVSVSTVPAP 120
Db      61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQSPVSVSTVPAP 120

Qy      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 171
Db      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 171

Qy      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 180
Db      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 180

Qy      172 ----- 171
Db      172 ----- 171

Qy      181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFFSVLLETAASLP 240
Db      181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFFSVLLETAASLP 240

Qy      172 ----- 171
Db      172 ----- 171

Qy      241 LSAAGSKEHYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLTLDRLDTEFSELEYSEM 300
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Qy      172 ----- 171
Db      172 ----- 171

Qy      301 GSSFVSVPKASAVIVANPREBIIIVKNKDEBEKLVSNILHNQQLPTALTATKLKVEDEVV 360
Db      301 GSSFVSVPKASAVIVANPREBIIIVKNKDEBEKLVSNILHNQQLPTALTATKLKVEDEVV 360

Qy      172 ----- 171
Db      172 ----- 171

Qy      361 SSEKAKDSFNKRVAVEAPMREYADFKPFRVWEVKDSKEDSMLAAGKIESNLESKV 420
Db      361 SSEKAKDSFNKRVAVEAPMREYADFKPFRVWEVKDSKEDSMLAAGKIESNLESKV 420

Qy      172 ----- 171
Db      172 ----- 171

Qy      421 DKKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFPNPAATESIATNIF 480
Db      421 DKKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFPNPAATESIATNIF 480

Qy      172 ----- 171
Db      172 ----- 171

Qy      481 PLLGDPSTENKTDKIEEKAQIVTEKNTSTKTSNPFLVAAQDSBTDYVTTDNLTKVTE 540
Db      481 PLLGDPSTENKTDKIEEKAQIVTEKNTSTKTSNPFLVAAQDSBTDYVTTDNLTKVTE 540

Qy      172 ----- 171
Db      172 ----- 171

Qy      541 EVVANMPEGLTPDLVQACESELNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 600
Db      541 EVVANMPEGLTPDLVQACESELNEVTGKIAVETKMDLVQTSVMQESLYPAAQICPSF 600

Qy      172 ----- 171
Db      172 ----- 171

Qy      601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKHEPENPPPYE 660
Db      601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKHEPENPPPYE 660

Qy      172 ----- 171
Db      172 ----- 171

Qy      661 EAMSVLKKVSGIKBEIKPENINAAQETAPYISACDLIKETKLSAEPAPDFSDYSE 720
Db      661 EAMSVLKKVSGIKBEIKPENINAAQETAPYISACDLIKETKLSAEPAPDFSDYSE 720

Qy      172 ----- 171
Db      172 ----- 171

Qy      721 MAKVEQVPDHSSELVEDSSDSEPVDLFSDDSIIPVQKQDETVMVLKESLTETSFEMI 780
Db      721 MAKVEQVPDHSSELVEDSSDSEPVDLFSDDSIIPVQKQDETVMVLKESLTETSFEMI 780

Qy      172 ----- 171
Db      172 ----- 171

Qy      781 EVENKEKLSALPPEGKPYLESFKLSLDNTKDTLPDPEVSTLSKKEKIPLOMEELSTAYY 840
Db      781 EVENKEKLSALPPEGKPYLESFKLSLDNTKDTLPDPEVSTLSKKEKIPLOMEELSTAYY 840
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Qy      172 ----- 171
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Qy      172 ----- 171
Db      901 ANAPDCAGSLPCTELPHDLISLKNIOPKVBEKISFSDDFSNGSATSATKVLPPDVSAAT 960
Qy      172 ----- 171
Db      961 QAEIESIVKPKVLVKEAEKCLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
Qy      190 FGASLFIILLSTVFSIVSTAYIALALISVTISFRIYKGVIOAIQKSDGEGHFRAYLSE 249
Db      1021 FGASLFIILLSTVFSIVSTAYIALALISVTISFRIYKGVIOAIQKSDGEGHFRAYLSE 1080
Qy      250 VAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVLMWVTFYVGLFNGLT 309
Db      1081 VAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVLMWVTFYVGLFNGLT 1140
Qy      310 LILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAMAKIQAKIPGLKRKAE 361
Db      1141 LILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAMAKIQAKIPGLKRKAE 1192

RESULT 14
US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429

Query Match      95.0%; Score 1756.9; DB 15; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy      1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60
Db      1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60

Qy      61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQSPVSVSTVPAP 120
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Qy      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 171
Db      121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSQAEVWTPPPAPAPAPPS 180

Qy      172 ----- 171
Db      172 ----- 171

Qy      181 SSGSVDETLPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFFSVLLETAASLP 240
Db      172 ----- 171

Qy      241 LSAAGSKEHYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLTLDRLDTEFSELEYSEM 300
Db      172 ----- 171

Qy      301 GSSFVSVPKASAVIVANPREBIIIVKNKDEBEKLVSNILHNQQLPTALTATKLKVEDEVV 360
Db      301 GSSFVSVPKASAVIVANPREBIIIVKNKDEBEKLVSNILHNQQLPTALTATKLKVEDEVV 360
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QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPERVWEVKDSKEDSMLAAGKIESNLESKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHEKDSSENDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTENKTDEKKIEBKAKQIVTEKNTSTKTSNPFVLAQDSETDVYTTNLTNLT 540
QY 172 ----- 171
Db 541 EVVANMPEGLTDLVQACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600
QY 172 ----- 171
Db 601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSEPLEASSVNYESIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSPDSEPDVLFSDSIPDPQKQDETVMVLVKESLTETSPESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPEGKPYLESFKLSLNDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSEAQIRETETSDSSPIEIIDFPPTLSSKTDSPSKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQPKVEKISFSDDFSKNGSATSKVLLLPDVSALAT 960
QY 172 ----- 171
Db 961 QAEIESIVKPLVKEAKKLPSTDEKDRSPSAIFSABELSKTSSVVDLLYWRDIKKTGVV 1020
QY 190 FGASLFLLSLTVFSIVSTAYTALALLSVTISFRIYKGVIOAIQKSDRGHPFRAYLESE 249
Db 1021 FGASLFLLSLTVFSIVSTAYTALALLSVTISFRIYKGVIOAIQKSDRGHPFRAYLESE 1080
QY 250 VAISELVQKYSNLSALGHVNCITIKELRLFLVDDLVDSLKFVLMVFTYVGALENGLTL 309
Db 1081 VAISELVQKYSNLSALGHVNCITIKELRLFLVDDLVDSLKFVLMVFTYVGALENGLTL 1140
QY 310 LILALISLSPVPIYERHQAQIDHYGLGNKVNKDMAKIOAKIPGLKRAE 361
Db 1141 LILALISLSPVPIYERHQAQIDHYGLGNKVNKDMAKIOAKIPGLKRAE 1192

```

```

RESULT 15
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (NAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

```

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; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match      95.0%; Score 1756.9; DB 16; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLDOSPLVSSSDSPRPQAPKQFVREPDEDEDEDEDEDEDEDEDEDEDELEELVKPKA 60
Db 1 MEDLDOSPLVSSSDSPRPQAPKQFVREPDEDEDEDEDEDEDEDEDEDEDELEELVKPKA 60
QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPAPRGPPLPAAPVAPRQPSWDPSPSVSSTVPAP 120
Db 61 AGLSAAPVPTAAGAPLMDFGNDFVPAPRGPPLPAAPVAPRQPSWDPSPSVSSTVPAP 120
QY 121 SPLSAAAASPSKLPEDDEPPARPPPPPPASVSQAEPPVMTTPAPAPAAPPS----- 171
Db 121 SPLSAAAASPSKLPEDDEPPARPPPPPPASVSQAEPPVMTTPAPAPAAPPS----- 171
QY 172 ----- 171
Db 172 ----- 171
QY 181 SSGSVDETLFALPAASEPVIRSAENMDLKEQPGNTISAGQEDFPFVLLTAAASLSLSP 240
Db 181 SSGSVDETLFALPAASEPVIRSAENMDLKEQPGNTISAGQEDFPFVLLTAAASLSLSP 240
QY 172 ----- 171
Db 241 LSAASFKEHEYLGNLSTVLPTBGTLOENVSEASKEVSEKAKTLLIDRDLTBSSELEYSEM 300
QY 172 ----- 171
Db 301 GSSFSVSKAESAVIVANPREBIIIVKNKDEEEKLVSNLILHNQQLPTALTTLKLVKEDEVV 360
QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPERVWEVKDSKEDSMLAAGKIESNLESKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHEKDSSENDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTENKTDEKKIEBKAKQIVTEKNTSTKTSNPFVLAQDSETDVYTTNLTNLT 540
QY 541 EVVANMPEGLTDLVQACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600
QY 172 ----- 171
Db 601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSEPLEASSVNYESIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSPDSEPDVLFSDSIPDPQKQDETVMVLVKESLTETSPESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPEGKPYLESFKLSLNDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSEAQIRETETSDSSPIEIIDFPPTLSSKTDSPSKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQPKVEKISFSDDFSKNGSATSKVLLLPDVSALAT 960

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Qy 172 -----TSVVLLYWRDIKKTGVV 189
Db 961 QAEIESIVPKVLVKEAEKKLPSPDEKDRSPSAIFSAELSKTSVVLLYWRDIKKTGVV 1020
Qy 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 249
Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 1080
Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVLMWVFTYVGALFNGLTL 309
Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVLMWVFTYVGALFNGLTL 1140
Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKKEAE 361
Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKKEAE 1192
```

Search completed: June 23, 2005, 10:34:33
Job time : 114.151 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:16:50 ; Search time 114.158 Seconds
(without alignments)
1223.045 Million cell updates/sec

Title: US-09-830-972-29-FUSED
Perfect score: 1850
Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1833.8	99.1	373	3	AAY53624 A bone ma
2	1833.8	99.1	373	3	AAY56969 Human MAG
3	1833.8	99.1	373	3	AAB24242 Human Nog
4	1833.8	99.1	373	4	AAB82350 Human NOG
5	1833.8	99.1	373	5	AAM47954 Human RTN
6	1833.8	99.1	373	5	ABP68601 Human pan
7	1833.8	99.1	373	5	ABH81079 Human neu
8	1833.8	99.1	373	7	AD163044 Human apo
9	1833.8	99.1	373	7	ADK67503 Human RTN
10	1833.8	99.1	373	8	ADP67235 Human NOG
11	1825.8	98.7	373	5	ABG30937 Human NOG
12	1756.9	95.0	1192	3	AAY56967 Human MAG
13	1756.9	95.0	1192	4	AAB82349 Human NOG
14	1756.9	95.0	1192	4	AAB82349 Human NOG
15	1756.9	95.0	1192	5	AAB82349 Human NOG
16	1756.9	95.0	1192	5	ABP68600 Human pan
17	1756.9	95.0	1192	5	ABH81078 Human neu
18	1756.9	95.0	1192	6	ABR59667 Human NOG
19	1756.9	95.0	1192	8	AD008103 Human pol
20	1756.9	95.0	1192	8	ADP45551 Human NOG
21	1756.9	95.0	1192	8	ADP67234 Human NOG
22	1756.9	95.0	1192	8	ADR13966 Human NOG
23	1749.9	94.6	1192	7	ADK67502 Human RTN
24	1749.9	94.6	1192	8	AD026400 Human tru
25	1749.3	94.6	1178	3	AAY71311 Human neu

26	1556.2	84.1	379	7	ADB85283	Adb85283 Rat fooc
27	1551.6	83.9	361	3	AAY71385	Aay71385 Alternati
28	1549.3	83.7	359	3	AAY71558	Aay71558 Rat Nogo
29	1546.3	83.6	360	3	AAY71383	Aay71383 Rat neuro
30	1546.3	83.6	360	5	ABB81076	Abb81076 Rat neuro
31	1480.5	80.0	360	4	AAE03987	Aae03987 Human gen
32	1478.8	79.9	1163	3	ADY71310	Ady71310 Rat neuro
33	1478.8	79.9	1163	3	ADY71310	Ady71310 Alternati
34	1478.8	79.9	1163	5	ABB81074	Abb81074 Rat neuro
35	1478.8	79.9	1163	8	ADO26399	Ado26399 Rat trunc
36	1478.8	79.9	1163	8	ADP45572	Adp45572 Rat NogoA
37	1476.8	79.8	1162	3	AAV71557	Aav71557 Rat Nogo
38	1475.2	78.7	1246	4	AAU33228	Aau33228 Novel hum
39	1455.3	78.7	1162	8	ADT89537	Adt89537 Mus muscu
40	1441.2	77.9	1163	8	ADO08105	Ado08105 Mouse pol
41	1324.8	71.6	291	4	AAM93484	Aam93484 Human pol
42	1324.8	71.6	291	8	ADL31138	Adl31138 Human pro
43	1234.5	66.7	973	8	ADQ16420	Adq16420 Fusion pr
44	1028	55.6	893	3	AA95012	Aay95012 Human sec
45	1028	55.6	983	6	ABU11573	Abu11573 Human MDD

ALIGNMENTS

RESULT 1
AAY53624
ID AAY53624 standard; protein; 373 AA.

AC AAY53624;

DT 22-FEB-2000 (first entry)

DE A bone marrow secreted protein designated BMS112.

KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint.

OS Homo sapiens.

PN WO9933979-A2.

PD 08-JUL-1999.

PF 18-DEC-1998; 98WO-US027008.

PR 30-DEC-1997; 97US-0068958P.

PR 24-SEP-1998; 98US-0101603P.

PR 30-SEP-1998; 98US-0102540P.

PA (CHIR) CHIRON CORP.

PI Lin H, Cao L;

DR WPI; 2000-038344/03.

DR N-PSDB; AA236230.

PT New isolated human polynucleotide and secreted proteins can induce

PT production of other cytokines in certain cell populations.

PS Claim 2; Page 74; 120pp; English.

CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow

CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or

CC cell differentiation activity (either inducing or inhibiting). They can

CC be used to support colony forming cells or factor-dependent cell lines,
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC deficiencies. In addition, they may be used to support the growth and
CC proliferation of erythroid progenitor cells, and to treat various
CC anaemias. They can have colony stimulating factor (CSF) activity and can
CC be used to support the growth and proliferation of myeloid cells such as
CC granulocytes, monocytes or macrophages, to prevent or treat myelo-
CC suppression, to support the growth and proliferation of megakaryocytes
CC and platelets, thereby allowing prevention or treatment of platelet
CC disorders such as thrombocytopenia, to support the growth and
CC proliferation of hematopoietic stem cells, either in place of or in
CC conjunction with platelet transfusions, to treat stem cell disorders,
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC repopulate the stem cell compartment after irradiation or chemotherapy.
CC They can be used for growth or differentiation of bone, cartilage, and
CC tendon, ligament, or nerve tissue, as well as for wound healing and
CC tissue repair and replacement, and in the treatment of burns, incisions
CC and ulcers, to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints
XX
SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 3; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTTPAPAPAPPSTPAAPKRRG 173
DB 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTTPAPAPAPPSTPAAPKRRG 180
QY 174 -----VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALLSVTISFRIYKG 228
DB 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALLSVTISFRIYKG 240
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVDSL 300
QY 289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAX 348
DB 301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAX 360
QY 349 IQAKIPGLKRAE 361
DB 361 IQAKIPGLKRAE 373

RESULT 2
AAV56969
ID AAV56969 standard; protein; 373 AA.
AC AAV56969;
XX
XX
DT 25-APR-2000 (first entry)
DE Human MAGI polypeptide variant.
XX
XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
XX stroke; cytostatic; cerebroprotective; neuroprotective; variant.
OS Homo sapiens.

XX WO200005364-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-GB002360.
XX
PR 22-JUL-1998; 98GB-00016024.
PR 19-JUL-1999; 99GB-00016898.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Michalovich D, Prinjha RK;
XX WPI; 2000-182693/16.
DR N-FSDB; AAZ56888.
XX
XX Novel polypeptides related to neuroendocrine-specific proteins and
PT polynucleotides useful for diagnosis of various diseases and for
PT treatment of cancer and neurological disorders.
XX
PS Claim 2; Page 22; 35pp; English.
XX
CC The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleotide is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents the human MAGI protein variant
XX
SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 3; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTTPAPAPAPPSTPAAPKRRG 173
DB 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTTPAPAPAPPSTPAAPKRRG 180
QY 174 -----VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALLSVTISFRIYKG 228
DB 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALLSVTISFRIYKG 240
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVDSL 300
QY 289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAX 348
DB 301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAX 360
QY 349 IQAKIPGLKRAE 361
DB 361 IQAKIPGLKRAE 373
RESULT 3
AAB24242
ID AAB24242 standard; protein; 373 AA.
XX
AC AAB24242;

Qy	289	KFAVLMMVFTYYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK	348
Dd	301	KFAVLMMVFTYYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK	360
Qy	349	IQAKTIPGLKRAE 361	
Dd	361	IQAKTIPGLKRAE 373	
 RESULT 4 AAB82350			
ID	AAB82350	standard; protein; 373 AA.	
AC	XX		
CC	AAB82350;		
DD	XX		
DT	23-JUL-2001	(first entry)	
XX	XX		
DE	XX	Human NOGO-B protein.	
XX	XX		
KW	NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;		
KM	stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;		
KW	neuromuscular disorder; psychiatric disorder; developmental disorder;		
KW	neuroprotective; nootropic; neuroleptic; antiparkinsonian;		
KW	cerebroprotective; neuroleptic; diagnosis; therapy.		
XX	XX		
OS	Homo sapiens.		
OS	WO200136631-A1.		
PX	XX		
PD	25-MAY-2001.		
XX	XX		
PF	14-NOV-2000; 2000WO-GB004345.		
XX	XX		
PR	15-NOV-1999; 99GB-00026995.		
PR	24-JAN-2000; 2000GB-00001550.		
XX	XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
PI	Michalovich D, Prinjha R;		
XX	XX		
DR	WPI; 2001-343822/36.		
DR	N-PSDB; AAF90325.		
XX	XX		
PT	New polypeptide designated NOGO-C is a splice variant of the human NOGO		
PT	gene and may be useful in the treatment of neural disorders including		
PT	Alzheimer's and Parkinson's diseases.		
XX	XX		
PS	Closure; Page 27-38; 25pp; English.		
XX	XX		
CC	The present sequence is that of human NOGO-B. NOGO-B is a previously		
CC	known splice variant of the human NOGO gene on chromosome 2p21. The		
CC	invention relates to a novel splice variant, NOGO-C (see AAB82348). It		
CC	provides NOGO-C polypeptides and polynucleotides, and methods for		
CC	producing such polypeptides by recombinant techniques. Also disclosed are		
CC	methods for utilising NOGO-C polypeptides and polynucleotides in the		
CC	treatment of diseases including neuropathies, spinal injury, brain		
CC	injury, stroke, neuronal degeneration, for example Alzheimer's disease		
CC	and Parkinson's disease, neuromuscular disorders, psychiatric disorders		
CC	and developmental disorders. Also provided are methods for identifying		
CC	agonists and agonists for use in treating conditions associated with NOGO		
CC	-C imbalance, and diagnostic assays for detecting diseases associated		
CC	with inappropriate NOGO-C activity or levels		
XX	XX		
SQ	Sequence 373 AA;		
 Query Match 99.1%; Score 1833.8; DB 4; Length 373; Best Local Similarity 96.5%; Pred. No. 9.7e-65; Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1			
Qy	1	MEDLOQSPLVSSSDSPRPQAFKYQFVRPEDEEEEEEEEEDEDDLEELVLRKPA	60
Dd	1	MEDLDQSLVSSSDSPRPQAFKYQFVRPEDEEEEEEEEEDEDDLEELVLRKPA	60

QY 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAFPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAFPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPSTPS 173
DB 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPSTPS 180
QY 174 -----VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
DB 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSL 300
QY 289 KPAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDAWAK 348
DB 301 KPAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDAWAK 360
QY 349 IOAKIPGLKRAE 361
DB 361 IOAKIPGLKRAE 373

RESULT 5
AAM47954
ID AAM47954 standard; protein; 373 AA.
AC AAM47954;
DT 04-MAR-2002 (first entry)
XX Human RTN4B SEQ ID NO 4.
DE Human; RTN4B.
KW Homo sapiens.
OS Homo sapiens.
XX CN1311439-A.
PN 05-SEP-2001.
PD 02-MAR-2000; 2000CN-00111791.
PF 02-MAR-2000; 2000CN-00111791.
PR (UYFU-) UNIV FUDAN.
PA Yu L, Fu Q, Zhao Y;
XX WPI; 2002-049934/07.
DR N-PSDB; ABA05903.
XX Human RTN 4B protein and coding sequence, its preparation and use.
PT Claim 5; Page 11 (Disclosure); 27pp; Chinese.
PS The invention relates to human RTN4B protein and coding sequence, useful for providing a cDNA sequence of human RTN4B. The protein is an isomer of RTN4 with RTN family members. The present invention also refers to CC polypeptide encoded by a nucleotide sequence and manufacturing method and CC application of the polypeptide and polynucleotide
SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 5; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 1; Mismatches 1; Indels 12; Gaps 1;
QY 1 MEDLQSLVSSSDSPRRPQPAFKYQFVREPEDEDEDEDEDEDELELEVLERKPA 60
|||||

DB 1 MEDLQSLVSSSDSPRRPQPAFKYQFVREPEDEDEDEDEDEDELELEVLERKPA 60
QY 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAFPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAFPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPSTPS 173
DB 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPSTPS 180
QY 174 -----VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
DB 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSL 300
QY 289 KPAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDAWAK 348
DB 301 KPAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDAWAK 360
QY 349 IOAKIPGLKRAE 361
DB 361 IOAKIPGLKRAE 373

RESULT 6
ABP68601
ID ABP68601 standard; protein; 373 AA.
AC ABP68601;
DT 14-JAN-2003 (first entry)
XX Human pancreatic cancer expressed protein SEQ ID NO 72.
DE Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW Cytostatic; tumour.
XX Homo sapiens.
OS WO200260317-A2.
PN 08-AUG-2002.
PD 30-JAN-2002; 2002WO-US002781.
PF 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
PA Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI WPI; 2002-627435/67.
XX N-PSDB; ABV94681.
DR New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer.
PT Claim 2; SEQ ID NO 72; 300pp + Sequence Listing; English.
PS The invention relates to an isolated polynucleotide (I) comprising: (a) CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

Dd 181 SSGSVVLLYYWRDIKKTGVFGASLFLLLSLTVFSVSVTAIYIALALLSVTISPRIYKG 240

Qy 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDVDSL 288

Dd 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDVDSL 300

Qy 289 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 348

Dd 301 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 360

Qy 349 IQAKIPGLKRAE 361

Dd 361 IQAKIPGLKRAE 373

RESULT 8

ADI63044

ID ADI63044 standard; protein; 373 AA.

XX AC ADI63044;

XX DT 22-APR-2004 (first entry)

XX DE Human apoptosis-associated protein SEQ ID 487.

XX KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;

XX KW antirheumatic; antiarthritic; dermatological; antiinflammatory;

XX KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;

XX KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;

XX KW autoimmune disease; degenerative disease; viral infection; leukaemia;

XX KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;

XX KW lupus; hepatitis; influenza viruses; Alzheimer's disease;

XX KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;

XX KW alcoholic liver disease; human.

XX OS Homo sapiens.

XX PN WO2003058021-A2.

XX PD 17-JUL-2003.

XX PF 13-JAN-2003; 2003WO-EP000270.

XX PR 11-JAN-2002; 2002DE-01000856.

XX PA (XANT-) XANTOS BIOMEDICINE AG.

XX PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;

XX DR WPI; 2003-542134/51.

XX PT New nucleic acids involved in apoptosis, useful for diagnosis and

XX PT treatment of e.g. tumors and degenerative disease, also related proteins,

XX PT antibodies and modulators.

XX PS Claim 1b; SEQ ID NO 487; 517pp; German.

XX CC This invention describes novel nucleic acid molecules that are associated

XX CC with apoptosis and encode a polypeptide and are derived from a normalised

XX CC gene library (embryonic or liver) or clone collections, and the extent of

XX CC apoptosis measured by cell death detection assay or the CPRG assay

XX CC (measuring loss of membrane integrity). The products of the invention

XX CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,

XX CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,

XX CC nootropic, anticonvulsant, antiparkinsonian, vasotropic,

XX CC cerebroprotective and antialcoholic activity and can be used for gene

XX CC therapy. The polynucleotides also related vectors, hosts (or their

XX CC extracts), encoded polypeptide (or their receptors) and/or agents that

XX CC inhibit their activity (including antisense sequences) are used for

XX CC treatment or prevention of tumours, autoimmune or degenerative diseases

XX CC and viral infections, specifically leukaemia, carcinoma, sarcoma,

XX CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection

XX CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or

CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver

CC disease. Detection of the polynucleotides and derived polypeptides can

CC also be used for diagnosis of these diseases. This sequence represents an

CC apoptosis-associated protein described in the invention.

XX SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 7; Length 373;

Best Local Similarity 96.5%; Pred. No. 9.7e-65;

Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDELELEVLKPKA 60

Dd 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDELELEVLKPKA 60

Qy 61 AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAAPPVAPERQPSWDSPSVSTVPAP 120

Dd 61 AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAAPPVAPERQPSWDSPSVSTVPAP 120

Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPOAEVWTPPAPAPAPPPST 173

Dd 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPOAEVWTPPAPAPAPPPST 173

Qy 174 -----VDLLYWRDIKKTGVFGASLFLLLSLTVFSVSVTAIYIALALLSVTISPRIYKG 228

Dd 181 SSGSVVLLYYWRDIKKTGVFGASLFLLLSLTVFSVSVTAIYIALALLSVTISPRIYKG 240

Qy 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDVDSL 288

Dd 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDDVDSL 300

Qy 289 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 348

Dd 301 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 360

Qy 349 IQAKIPGLKRAE 361

Dd 361 IQAKIPGLKRAE 373

RESULT 9

ADK67503

ID ADK67503 standard; protein; 373 AA.

XX AC ADK67503;

XX DT 06-MAY-2004 (first entry)

XX DE Human RTN-4B protein.

XX KW neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;

XX KW Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO2003089926-A2.

XX PD 30-OCT-2003.

XX PF 08-APR-2003; 2003WO-US008829.

XX PR 17-APR-2002; 2002US-0373284P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Yan R, Lu Y;

XX DR WPI; 2003-854033/79.

XX PT New polypeptide having BACE1 activity, useful in preparing a composition

XX PT for treating amyloidosis or Alzheimer's disease.

XX PS Claim 52; SEQ ID NO 8; 42pp; English.

FT	Peptide	180..193
FT	/note="Nogob (ASV) peptide, distinguishes Nogob from	
FT	.other "Nogo isoforms"	
FT	Peptide	272..285
FT	/note="Nogob (ASV) peptide"	
PX	WO200257483-A2.	
XX		
XX	25-JUL-2002.	
XX		
XX	18-JAN-2002; 2002WO-GB000228.	
PR	18-JAN-2003; 2001GB-00001312.	
XX	(GLAX) GLAXO GROUP LTD.	
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
XX		
PI	Blackstock WP; Hale RS, Prinjha R, Rowley A;	
DR	WPI; 2002-599722/64.	
N-	PSDB; ABK90133.	
XX		
PT	Identifying modulators of Nogo or BACE activity for treating acute	
PT	neuronal injuries, neoplastic or dysproliferative disorders, comprises	
PT	providing and monitoring interaction between Nogo and BACE polypeptides.	
XX		
XX	Example 1; Page 25; 68pp; English.	
XX		
CC	The present invention relates to a new method of identifying modulators	
CC	of Nogo function or BACE activity. The method involves providing Nogo and	
CC	BACE polypeptides capable of binding with each other, monitoring the	
CC	interaction between these polypeptides, and determining if the test agent	
CC	is a modulator of Nogo or BACE activity. The method is useful in treating	
CC	acute neuronal injuries, such as spinal or head injury, stroke,	
CC	peripheral nerve damage, and in neoplastic (e.g. glioblastomas,	
CC	neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.	
CC	cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue	
CC	hypertrophy) of the central nervous system. The BACE polypeptide is	
CC	useful in screening methods to identify agents that may act as modulators	
CC	of BACE activity and in particular agents that may be useful in treating	
CC	Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,	
CC	and the polynucleotide encoding the BACE polypeptide are useful in	
CC	manufacturing a medicament for the treatment or prevention of disorders	
CC	responsive to the modulation of Nogo activity, in alleviating the	
CC	symptoms or improving the condition of a patient suffering from this	
CC	disorder, in axon regeneration, or in preventing metastasis or spreading	
CC	of a cancer. The polynucleotide may also be an essential component in	
CC	assays, a probe, in recombinant protein synthesis, and in gene therapy	
CC	techniques. The present amino acid sequence represents the human Nogob	
CC	protein of the invention	
XX		
SQ	Sequence 373 AA;	
	Query Match	98.7%; Score 1825.8; DB 5; Length 373;
	Best Local Similarity	96.0%; Pred. No. 2e-64;
	Matches 358; Conservative	1; Mismatches 2; Indels 12; Gaps 1
QY	1 MEDLDQSPLVSSSDSPRRPQAFKYQFVRPEDEEEEEEDDEDLEEVLERKPA 60	
Db	1 MEDLDQSPLVSSSDSPRRPQAFKYQFVRPEDEEEEEEDDEDLEEVLERKPA 60	
QY	61 AGLSAAPVPTAAPAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQSWDPSPVSSVTVPAP 120	
Db	61 AGLSAAPVPTAAPAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQCPWPSPSVSSTVPAP 120	
QY	121 SPLSAAAAYSPLKPEDDDEFPARP PPPPPASVSQAEPVMTTPAPAAPAPPS----- 173	
Db	121 SPLSAAAAYSPLKPODDDFARP PPPPPASVSQAEPVMTTPAPAAPAPPSPTAAPKRGR 180	
QY	174 -----VDLLLYWRDIKTGTGVFGASLFLLLSLTVFSIVSVTAYIALALUSVTISFRYYKG 228	
Db	181 SSGSVVVDLLLYWRDIKTGTGVFGASLFLLLSLTVFSIVSVTAYIALALUSVTISFRYYKG 240	

CC	injury, stroke or a demyelinating disease selected from multiple
CC	sclerosis, monophasia demyelination, encephalomyelitis, multifocal.
CC	leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC	pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC	Spongy degeneration, Alexander's disease, Canavan's disease,
CC	metachromatic leukodystrophy, viral infection and Krabbe's disease
XX	
SQ	Sequence 1192 AA;
	Query Match 95.0%; Score 1756.9; DB 4; Length 1192;
	Best Local Similarity 30.3%; Pred. No. 8.5e-61;
	Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;
Qy	1 MEDLDQSLVSSSDSPRPQAFKYQFVREPEDEEEEEDEDELELEVLERKPA 60
Db	1 MEDLDQSLVSSSDSPRPQAFKYQFVREPEDEEEEEDEDELELEVLERKPA 60
Qy	61 AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPRQPSWDSPSVSTVPAP 120
Db	61 AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPRQPSWDSPSVSTVPAP 120
Qy	121 SPLSAAAVSPSKLPEDDEPPARPPPPASVPOAEPVWTPPPAPAPAAPPS- 171
Db	121 SPLSAAAVSPSKLPEDDEPPARPPPPASVPOAEPVWTPPPAPAPAAPPS- 180
Qy	172 ----- 171
Db	181 SSGSVDETFLALPAASEBFINRSSAENMDLKEQPGNTISAGQEDFPFVLLTAASLP 240
Qy	172 ----- 171
Db	241 LSAASFKEHYGLNLSVTLPTGTLQENVSEASKEVSEKATLLIDRLDTFSELEYSEM 300
Qy	172 ----- 171
Db	301 GSSFSPVSKAESAVIVANPREEIIIVKNKDEEKLVSNNILHNQQLPTALTKLVEDEV 360
Qy	172 ----- 171
Db	361 SSEKAKDSFNEKRVAVEAPMREYADFPPFVWEVKDSKEDSDMLAAGGKIESNLESKV 420
Qy	172 ----- 171
Db	421 DKKCFADSLBOTNHEKSESSNDSTSPSTPEGIKDRSGAVITCAPFNPAATESIANNIP 480
Qy	172 ----- 171
Db	481 PLLGDPTSENKTDKKIEEKKAIQVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540
Qy	172 ----- 171
Db	541 EVVANMPEGLTPDLIVQACESELNEVTGTKIAYETKMDLVQTSVWQESLYPAAQLCPSF 600
Qy	172 ----- 171
Db	601 EESDATSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNVYSIKHEPENPPPYE 660
Qy	172 ----- 171
Db	661 EAMSVSLKKVSGIKKEEIKPENINAALQETAPYISACDLIKETKLSAEPAPDFSDYSE 720
Qy	172 ----- 171
Db	721 MAKVEQVPDPHSELVEDSSPDSBPVDLFDSDSIFDPVQKQDETVMLVKESLTETSFMSI 780
Qy	172 ----- 171
Db	781 EYENKEKLSALPPSGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
Qy	172 ----- 171
Db	841 SNDDLFTISKEAOIRETETFDSSPIEIIIDEPTLLISKTDSFSLAREYTDLEVSHKSEI 900

QY	172	-----	171
Db	901	ANAPDAGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPVSALAT	960
QY	172	-----	171
Db	961	QAEIESIVKPKVLKAEKKLPDTEKEDRSPSAISFAELSKTSVDDLLYWRDIKKTGVV	1020
QY	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYLESE	1080
QY	250	VAISEELVQKYSNSALGHVNNCTIKELRRLFLVDLVDLSLKFVLMVFTVYGALFNGLT	309
Db	1081	VAISEELVQKYSNSALGHVNNCTIKELRRLFLVDLVDLSLKFVLMVFTVYGALFNGLT	1140
QY	310	LILALISLFSVPVITYERHQAIIDHYLGLANKNVKDAMAKIQAKIPGLKRAE	361
Db	1141	LILALISLFSVPVITYERHQAIIDHYLGLANKNVKDAMAKIQAKIPGLKRAE	1192
RESULT 15			
Db	ABG30938		
ID	ABG30938	standard; protein; 1192 AA.	
XX	AC	ABG30938;	
XX	AC		
DT	21-OCT-2002	(first entry)	
XX		Human NogoA protein.	
XX		Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;	
KW		stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;	
KW		neuroblastoma; hyperproliferative disorder; dysproliferative disorder;	
KW		cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;	
KW		tissue hypertrophy; central nervous system; axon regeneration; NogoA;	
KW		Nogo-associated disease; metastasis.	
XX			
OS		Homo sapiens.	
XX			
FN		WO200257483-A2.	
XX			
PD		25-JUL-2002.	
XX			
PF		18-JAN-2002; 2002WO-GB000228.	
XX			
PR		18-JAN-2001; 2001GB-00001312.	
XX			
FA		(GLAXO) GLAXO GROUP LTD.	
PA		(SMIK) SMITHKLINE BEECHAM PLC.	
XX			
PI		Blackstock WP, Hale RS, Prinjha R, Rowley A;	
XX			
DR		WPI; 2002-599722/64.	
DR		N-PSDB; ABK90134.	
XX			
PT		Identifying modulators of Nogo or BACE activity for treating acute	
PT		neuronal injuries, neoplastic or dysproliferative disorders, comprising	
PT		providing and monitoring interaction between Nogo and BACE polypeptides.	
XX			
PS		Disclosure; Page 59-62; 68pp; English.	
XX			
CC		The present invention relates to a new method of identifying modulators	
CC		of Nogo function or BACE activity. The method involves providing Nogo and	
CC		BACE polypeptides capable of binding with each other, monitoring the	
CC		interaction between these polypeptides, and determining if the test agent	
CC		is a modulator of Nogo or BACE activity. The method is useful in treating	
CC		acute neuronal injuries, such as spinal or head injury, stroke,	
CC		peripheral nerve damage, and in neoplastic (e.g. glioblastomas,	
CC		neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.	
CC		cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue	
CC		hypertrophy) of the central nervous system. The BACE polypeptide is	
CC		useful in screening methods to identify agents that may act as modulators	

CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents the human NogoA
CC protein of the invention

XX Query Match 95.0%; Score 1756.9; DB 5; Length 1192;
SQ Best Local Similarity 30.3%; Pred. No. 8.5e-61;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLQSPVLSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEELERKPA 60
DB |||||
QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERPQSWDPSPVSTVPAP 120
DB |||||
QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERPQSWDPSPVSTVPAP 120
DB |||||
QY 121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSPQAPVWTPPAPAPAPPS----- 171
DB |||||
QY 121 SPLSAAVSPSKLPEDDEPPAPPPPPPPASVSPQAPVWTPPAPAPAPPSPPAPAKRGG 180
DB |||||
QY 172 ----- 171
DB 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQDFPVLLETAASLPSLSP 240
QY 172 ----- 171
DB 241 LSAASFKEHYLGNLSTVLPTGTLOENVSEASKEVSEKAKTLILDRDLTFESELEYSEM 300
QY 172 ----- 171
DB 301 GSSFVSFPAESAVIVANPREELIIVKNKDEBKLYSNLILHNQBELPTALTCLKVKEDEVV 360
QY 172 ----- 171
DB 361 SSEKAKDSFNEKRVAVEAPRMREYADFKFERVWEVKDSKEDSMDLAAGKIESNLESKV 420
QY 172 ----- 171
DB 421 DKCFADSLQTNHEKQSSNDNTSFPSTPEGIKDRPGAYITCAPFPNPAATESIATNIF 480
QY 172 ----- 171
DB 481 PLLGDPTSENKTEKKIEBKAKQIVTEKNTKTSTNSPFLVAAQDSETDYVTTDNLTKYTE 540
QY 172 ----- 171
DB 541 EYVANMPEGLTDLVQACESELNEVTGKIAYETKMDLVQTSSEVMQESLYPAAQLCPSPF 600
QY 172 ----- 171
DB 601 ESEATPSVPLDIVMEAPLNSAVFSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
QY 172 ----- 171
DB 661 EAMSVLKKVGIKEIKEPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
DB 721 MAKVEQVPDHSVELDSSPDSEPVDLFSDDSIPDVQPKQDETVMVKESLTETSFESMI 780
QY 172 ----- 171
DB 781 EYENKEKLSALPEGKPKYLFKLSLNDNTKTLPLDDEVSTLSKKKEKTLQMEELSTAVY 840

QY 172 ----- 171
DB 841 SNDDLFIISKEAQIRETETFSDDSSPIEIIDERFPTLISSKTDSPSKLAREVTDLEVSHKSEI 900
QY 172 ----- 171
DB 901 ANAPDAGSLPCTELPHDLNKLNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALAT 960
QY 172 -----TSVVDLILYWRDIKKTGV 189
DB 961 QAEIESIVKPKVLVKEAEKLPFSDTEKEDRSPSAIFSALSKTSVVDLILYWRDIKKTGV 1020
QY 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 249
DB 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 1080
QY 250 VAISELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMMVFTYVGALFNGLT 309
DB 1081 VAISELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMMVFTYVGALFNGLT 1140
QY 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 361
DB 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192

Search completed: June 23, 2005, 10:52:04
Job time : 118.158 secs

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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:29:31 ; Search time 25.0347 Seconds
(without alignments)
1387.446 Million cell updates/sec

Title: US-09-830-972-29-FUSED
Perfect score: 1850
Sequence: 1 MEDLQSPVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRYAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.7	44.7	776	2 A46583	neuroendocrine-spe
2	684.2	37.0	208	2 I60904	neuroendocrine-spe
3	666	36.0	267	2 A60021	tropomyosin-relate
4	454.3	24.6	2484	2 T26216	hypothetical prote
5	447	24.2	2607	2 T26215	hypothetical prote
6	353.5	19.1	222	2 T26213	hypothetical prote
7	275.1	14.9	1173	2 T31421	C-terminal domain-
8	266	14.4	1206	2 S24407	formin isoform IV
9	266	14.4	1468	2 S11515	formin - mouse
10	264.1	14.3	1058	2 T13286	cappuccino gene pr
11	262.4	14.2	1611	2 T38236	hypothetical prote
12	260.9	14.1	760	2 F86387	probable Pto kinase
13	257.1	13.9	3511	2 A59295	unconventional myo
14	256.5	13.9	1255	2 T31065	diaphanous protein
15	255.5	13.8	3530	2 A59266	unconventional myo
16	253.8	13.7	1132	2 A35098	MHC class III hist
17	253.6	13.7	1201	2 G86441	unknown protein [l
18	250.9	13.6	1100	2 JC8033	leukocyte formin p
19	250.4	13.5	880	2 D89756	protein T23E7.2b [
20	250	13.5	980	2 J54986	regulatory protein
21	247.7	13.4	1015	2 JC6552	DNA topoisomerase
22	247.5	13.4	731	2 B86369	hypothetical prote
23	247.3	13.4	980	2 G75523	probable cell divi
24	247.2	13.4	1047	2 A55617	masquerade precurs
25	247	13.4	2090	2 S26058	probable transform
26	244.8	13.2	1127	2 T32404	hypothetical prote
27	244.8	13.2	1375	2 S48375	hypothetical prote
28	243.6	13.2	1721	1 I38902	retinoblastoma bin
29	243.4	13.2	3938	2 T42761	Bassoon protein -

30	243.3	13.2	708	2 D96711	hypothetical prote
31	243.3	13.2	786	2 A34666	progesterone recep
32	243	13.1	907	2 E96636	hypothetical prote
33	242.9	13.1	1634	2 T26517	hypothetical prote
34	242.6	13.1	716	2 T26998	hypothetical prote
35	241.5	13.1	933	1 ORHUP	progesterone recep
36	239.2	12.9	449	2 S16748	proline-rich prote
37	239.1	12.9	930	2 A25923	progesterone recep
38	238.7	12.9	1706	2 I84499	zinc finger protei
39	238.3	12.9	3149	1 Q0BE8	BPLF1 protein - hu
40	237	12.8	1137	2 A86335	T20H2.9 protein -
41	236.9	12.8	710	2 D96728	hypothetical prote
42	236.7	12.8	2649	2 T51023	hypothetical prote
43	235.6	12.7	765	2 T49592	neurofilament trip
44	235.2	12.7	1953	2 S63244	BN11 protein - yea
45	235.1	12.7	534	2 S21961	proline-rich prote

ALIGNMENTS

RESULT 1

A46583
neuroendocrine-specific protein, splice form A - human
N:Contains: neuroendocrine-specific protein, splice form B
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: A46583; I60903
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Ve
J. Biol. Chem. 268, 13439-13447, 1993
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec
A:Reference number: A46583; MUID:93293865; PMID:7685762
A:Accession: A46583
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-776 <ROE1>
A:Cross-references: UNIPROT:Q16799; GB:I10333; NID:G307306; PIDN:AAA59950.1; PID:G307307
A:Accession: I60903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 421-776 <ROE2>
A:Cross-references: GB:I10334; NID:G307308; PIDN:AAA59951.1; PID:G307309
C:Genetics:
A:Gene: GDB:RTN1; NSP
A:Cross-references: GDB:203968; OMIM:600865
A:Map position: 14q21-14q22
Query Match 44.7%; Score 827.7; DB 2; Length 776;
Best Local Similarity 27.1%; Pred. No. 4.8e-20;
Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;
QY 6 QSP----- 9
DB 70 QSPVAMEASTGAGVSSAMDTFTTSKDGSCVTSLSIDICYPQSDSTFTGILQK 129
QY 10 -----VSSDSPR-----POP----- 21
DB 130 ENGHVTISEPSELGTGPGSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM 189
QY 22 ---AFKYQVVRPEDEEEDEDEDELE----- 50
DB 190 KAAYKVIDITRPEVKHQEHPELEDKDLDFKNKDTISIKPEGVREPDPAPVEGKI 249
QY 51 -----ELE----- 53
DB 250 IKDHLLSESTFAPYIDDLSEQRAPQITTPVKITLITEPSVETTTQETPEKQDICKL 309
QY 54 -----VLERPAAGLS-- 64
DB 310 PSPDTVPTVTVSEPEDDPSGSIPTPSSGTPESAESQKGSISELITAIKEAKGLSVE 369
QY 65 ----RAPV-----PTAPAGAPL----- 78

Db 370 TAENRPFVGLADRPVVKARSGPPTIP-----SPLDHEASSAESGDSIELVSEDPMAAEDA 426

Qy 79 -----MDFGNDFFPAPRGPPLPAPV-----APE 103

Db 427 LPSGYVSFGHVGPP-----PSPASPSIQYSIILREAREALDSELIIESCDASASESPK 482

Qy 104 RQ---PSWDSPVVS-----STVPAPSPLSMAAVSP 130

Db 483 REQDSPMPKPSALDAIREETGVRAERAPSRRLAEPGSLFDPSTEPQGP-----534

Qy 131 SKLPED-----EPPAPRPPPPASVSPQAEVPWTPPAP-APAAPP-----STSVVDLL 178

Db 535 -ELPPDGDGALEPETMLPKRPEDSSNQSPAAATKGPFLGPGAPPLFLFNKQKAIDL 593

Qy 179 YNRDIKKTGVFGASLFLLLSVTSIVSYAVIALALLSVTISPRIYKGVTOAKSD 238

Db 594 YNRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISPRIYKSVIQAQVKTDE 653

Qy 239 GHPPFRAYLESEVAISELQKYSNSALGHVNCITIKELRRLFLVDLLVDSLKFAVLMWVFT 298

Db 654 GHPPFRAYLEITLSQEQIKYQKTDCLQFYVNSTLKELRRLFLVDLLVDSLKFAVLMWLLT 713

Qy 299 YVGALENGTLTILALISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOAKIPGLKR 358

Db 714 YVGALENGTLTLLMAVSMFTLPVVYVVKHQAQIDQYGLVTRTHINAVVAKIOAKIPGAKR 773

Qy 359 KAE 361

Db 774 HAE 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; Van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16739; GB:L10335; NID:g307310; PIDN:AAAS9952.1; PID:g307311

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203969; OMIM:600865

A:Map position: 14q21-14q22

Query Match 37.0%; Score 684.2; DB 2; Length 208;

Best Local Similarity 62.4%; Pred. No. 1.3e-16;

Matches 131; Conservative 35; Mismatches 36; Indels 8; Gaps 1;

Qy 152 SPOAEPVWTPPAPAPAPPSSTVVDLLYWRDIKKTGVFGASLFLLLSVTSIVSYAVT 211

Db 7 STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAY 58

Qy 212 IALALLSVTISPRIYKGVTOAKSDGHPFRAYLESEVAISELVQKYSNSALGHVNC 271

Db 59 LALAALSATISPRIYKSVLQAVQKTDGHPFRAYLEITLSQEQIKYQKTDCLQFYVNST 118

Qy 272 IKELRRLFLVDLLVDSLKFAVLMWVTVYVGALENGTLTILALISLFSVPVIYERHOAQI 331

Db 119 LKELRRLFLVDLLVDSLKFAVLMWLLTYVGALENGTLTLLMAVSMFTLPVVYVVKHQAQI 178

Qy 332 DHYGLANKNVKDMAKIOAKIPGLKRAE 361

Db 179 DQYGLVTRTHINAVVAKIOAKIPGAKRAE 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C:Accession: A60021

R:Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A:Reference number: A60021; MUID:91278684; PMID:1647480

A:Accession: A60021

A:Molecule type: mRNA

A:Residues: 1-267 <WIE>

A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550

C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 36.0%; Score 666; DB 2; Length 267;

Best Local Similarity 66.1%; Pred. No. 1e-15;

Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

Qy 172 TSVVDLLYWRDIKKTGVFGASLFLLLSVTSIVSYAVIALALLSVTISPRIYKGVIQ 231

Db 10 SQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISPRIYKSVIQ 69

Qy 232 AIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDLLVDSLKFA 291

Db 70 AVQKTDGHPFRAYLEITLSQEQIKYQKTDCLQFYVNSTLKELRRLFLVDLLVDSLKFA 129

Qy 292 VLMWVTVYVGALENGTLTILALISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOA 351

Db 130 VLMWLLTYVGALENGTLTLLMAVSMFTLPVVYVVKHQAQDQYGLVTRTHINTVVAKIOA 189

Qy 352 KIPGLK 357

Db 190 KIPGAR 195

RESULT 4

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26216

R:Ainscough, R.

Submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26216

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2484 <WIL>

A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3c

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 24.6%; Score 454.3; DB 2; Length 2484;

Best Local Similarity 15.7%; Pred. No. 4.2e-06;

Matches 126; Conservative 79; Mismatches 142; Indels 457; Gaps 18;

Qy 1 MEDLQSPVLSVSSDSPPR-----PQAFKYOQV-----REPDEEEE 38

Db 1679 VESLERPLTIITQKPKPEKPTDIGALSPLSNTLAEYEVPMQSVPHSPQEQEEI 1738

Qy 39 E-----EEE 42

Db 1739 EALSEIIEPQAMKEVPESAPEKDNESLEAPIINEPIRRLVETKIMGPGKSLNED 1798

Qy 43 EDEDED-----48

Db 1799 NDDDDGSECLSDIGLSERTIQRTNTSIDPSIRDSFSSISSFGDROKFRTAENIRQ 1858

Qy 49 -----LEELEVLER 57

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Db 1859 DLLPFQSSVSYLRSSPNPSSQQLLVNLSMDSPDLSNAPPVGVGFNTAQFLEKQOEDR 1918
QY 58 KPAAG-----LSAAPV----- 68
Db 1919 PSAEGSIDSSGPEKVDHEGLDEFAAPVHDPMQKSVFGSLGDDMKPGSQDDGFVFIERN 1978
QY 69 -----PTAPAGAPLM----- 79
Db 1979 EANEATLKKQKMSHHNDVIEKNYFNDNAPTAALLESPIAEARKLVQDAVESASEYKK 2038
QY 80 -----DFGNDVFVPPA----- 89
Db 2039 QAVDSGEIGRELLDNVEQKIEQVKPEIVDSLHKAYDGVGFVHETVPNAVDDFVREAEK 2098
QY 90 --PRGLP-----AAPP-----VAP--ERQP----- 106
Db 2099 QLPESVPKEIETPEPLVDIHDVTKVHDEVNFLRREPTPETDDVAPLSDDKPQFGN 2158
QY 107 -----SWDPSVSTVPAPSPLSAAAVSPSK 132
Db 2159 QTPEDETTFDRKGPIITPEEVEKAAQNNLDDFDPLVTSNTGAAGAAVGAAGAAVES 2218
QY 133 LPEDD-----EPPARPPPPP-----PASV-----SPOAEP-----V 158
Db 2219 LTEEMFGHQKFTVPRPTPKDISDEDKPSTVNLGSPSHHSHSPSSPHHSILKHGDA 2278
QY 159 W-----TPAPAPAPSP-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVVTVYSL 2328
Db 2279 WIDFKTVPPC-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVVTVYSL 2328
QY 214 LALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITK 273
Db 2329 LLALGAAAGFRVFKVEAQIKKTDSEHPFSEILAQDLTLPOEKVHAQADVFEHATCIAN 2388
QY 274 ELRRLPLVDLSDKFAVLMVFTVVGALFNGLTLLIALLSLFSPVPIYERHQAIQIDH 333
Db 2389 KUKGLVFPSPLESIKFGLVLSLTIASWFGFTLAILGLLGVSVPKYESQAEIDP 2448
QY 334 YLGLANKVNDAMAKIQAKIPGLK 357
Db 2449 HLATISGHLKNQNIIDEKLPFLR 2472
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RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CA01522.2; GSPDB:GN00023; CESP:W0
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 24.2%; Score 447; DB 2; Length 2607;
Best Local Similarity 14.0%; Pred. No. 8.5e-06;
Matches 128; Conservative 79; Mismatches 150; Indels 560; Gaps 18;
QY 1 MEDLDQSLVSSSDSPRR-----PQAPFKYQFV-----REPDEDEEE 38
Db 1679 VESLERPLTIITQKPEKPTEDIGALSPISPTLAEYEVPMQSDVPHSPQEQEIEI 1738
QY 39 E-----EEE 42
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Db 1739 EALSELIEBPQAMKEVKEKPVESAPEKDNESLEAPELINEPIRRLVLTETKMGPKSLNED 1798
QY 43 EDEDED----- 48
Db 1799 NDDDDGSGCLSDIGLDSERTIQRFNTSIDPSIRRDSPSSISFGDRQKFRTAIENIRQ 1858
QY 49 -----LEELEVLER 57
Db 1859 DLLPFQSSVSYLRSSPNPSSQQLLVNLSMDSPDLSNAPPVGVGFNTAQFLEKQOEDR 1918
QY 58 KPAAG-----LSAAPV----- 68
Db 1919 PSAEGSIDSSGPEKVDHEGLDEFAAPVHDPMQKSVFGSLGDDMKPGSQDDGFVFIERN 1978
QY 69 -----PTAPAGAPLM----- 79
Db 1979 EANEATLKKQKMSHHNDVIEKNYFNDNAPTAALLESPIAEARKLVQDAVESASEYKK 2038
QY 80 -----DFGNDVFVPPA----- 89
Db 2039 QAVDSGEIGRELLDNVEQKIEQVKPEIVDSLHKAYDGVGFVHETVPNAVDDFVREAEK 2098
QY 90 --PRGLP-----AAPP-----VAP--ERQP----- 106
Db 2099 QLPESVPKEIETPEPLVDIHDVTKVHDEVNFLRREPTPETDDVAPLSDDKPQFGN 2158
QY 107 -----SWDPSVSTVPAPSPLSAAAVSPSK 132
Db 2159 QTPEDETTFDRKGPIITPEEVEKAAQNNLDDFDPLVTSNTGAAGAAVGAAGAAVES 2218
QY 133 LPEDD-----EPPARPPPPP-----PASV-----SPOAEP-----V 158
Db 2219 LTEEMFGHQKFTVPRPTPKDISDEDKPSTVNLGSPSHHSHSPSSPHHSILKHGDA 2278
QY 159 W-----TPAPAPAPSP-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVVTVYSL 2328
Db 2279 WIDFKTVPPC-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVVTVYSL 2328
QY 171 ----- 170
Db 2339 HVKHKRFRWNEEQATTMSKLGAVGRGLYALIAFTVNLVRLGNLVALVGVAVSAHEAY 2398
QY 171 -----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYTALALLSVT 220
Db 2399 KLTSSGVLRRKKEVLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVVTVYSL 2458
QY 221 ISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITKELRRLFL 280
Db 2459 AGFRVFKVVEAQIKKTDSEHPFSEILAQDLTLPOEKVHAQADVFEHATCIANKKLVF 2518
QY 281 VDDLVDLSLKFAVLMVFTVVGALFNGLTLLIALLSLFSPVPIYERHQAIQIDHVLGLANK 340
Db 2519 VESPLESIKFGVLVLSLTIASWFGFTLAILGLLGVSVPKYESQAEIDPHLATISG 2578
QY 341 NVKDAMAKIQAKIPGLK 357
Db 2579 HLKNVQNIIDEKLPFLR 2595
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RESULT 6

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T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26213
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <WIL>
```

A:Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP.W06A7.3b
A:Map position: 5
A:Introns: 27/1; 77/2; 201/2

Query Match 19.1%; Score 353.5; DB 2; Length 222;
Best Local Similarity 32.2%; Pred. No. 2.6e-05;
Matches 65; Conservative 48; Mismatches 84; Indels 5; Gaps 1;

QY 156 EVWTPAPAPAPSTSVVLLYWRDIKKTGVFGASLFLSLTTFVSIVSVTAIYALA 215
DB 14 QPTWVPATDFG-----KILDVIYWRDAKSAIVLSALLVFLAKYPLLTWVYSLIL 68

QY 216 LLSVTISFRIYKGVIOAKIOKSEGEHPFRAYLSEVAISEELVQKYSNSALGHVNCITKEL 275
DB 69 ALGAAAGFRVFKVRAQIKKTSSEHPFSEILAQDLTLPOEKVHAQADVEHATCIANKL 128

QY 276 RRLFLVDLVDLSLKFAVLMMVFTYVGCALFNGLTLLTILALISLFSFVPIYERHQAQIDHYL 335
DB 129 KKLVFVESPLESIKGLVLSLTYTASWFSGFTLAILGLLVFSVPKVIYESNQEAIDPHL 188

QY 336 GLANKNVKDMAKIOAKIPLK 357
DB 189 ATISGHLKNVQNIIDEKLPFLR 210

RESULT 7
T31421
C:terminal domain-binding protein rA1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31421
R:Juryev, A.; Patturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <YR>
A:Cross-references: UNIPROT:Q63624; EMBL:U49056; NID:g1438531; PID:g1438532; PIDN:AAC526
A:Experimental source: hippocampus

Query Match 14.9%; Score 275.1; DB 2; Length 1173;
Best Local Similarity 10.8%; Pred. No. 0.77;
Matches 130; Conservative 43; Mismatches 93; Indels 939; Gaps 30;

QY 3 DLDQQLV----- 10
DB 52 DRDMPPLVPSLLPLRAWRTKTVSPQSHARPACSRHLLTLTGDCGAPPPAPSSGS 111

QY 11 -----SSDSPPRPQP-----AF-----KYQ----- 26
DB 112 SSPSPSPSSSPSPPPPPPPPPALPAPRFDIYDPFHTDEAYSPPPAPEQKYDPFEAT 171

QY 27 -----FVREPEDEEEEEEEED----- 44
DB 172 GSNPSSSGTSPSEEEEEEEEGLSQSIRRISETLAGIYDNNLSQDPFGDDSPHR 231

QY 45 ----- 44
DB 232 EPPPPQTLGAPGTPQADSTRAEAGPRRRVVFVGPAAEACLEGKYSVEVVTAGGPALEPL 291

QY 45 -----EDEDLEBELEVL-----RKPAAG-----LSAAPVPTTAPACAPLM 79
DB 292 PPLPPTDPEIERGEIVQPEEPRVAVSLFRAARPPQPPASVATLASVAAPAAAPASAPRA 351

QY 80 DGNDFV-----PPAP----- 91
DB 352 PEGDDFLSLHADSDEGALQVDLGEPPAPPAADARWGGLDLRRKILTORRERYORSASP 411

QY 92 GELPAPPPVAPERQSPWDPSPVSS----- 115
DB 412 GPPPAKKARRERQSGDPAPDPDSTWEAKKHSRERKLGSHSTARRRSRSTRSRSR 471

QY 116 ----- 115
DB 472 SADRRRGSHRSRERKRRRRRRSASPPPAASSSSSSSRRHRHGRKREGGKKKKGRSRA 531

QY 116 -----TVAPSPLS----- 124
DB 532 EKRSGLKLPAPVPPSGSDRRRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKTEPRA 591

QY 125 -----AAAVSPS----- 131
DB 592 PSPAPAVSPKGEVLVDSEGLSADERGA GDKDRRSGAASSSSSSSRKASRRKALDGDG 651

QY 132 -----KLPEDEP----- 139
DB 652 RDRDRSSKKRPTPKDSAPFGALPKAPPSSSSSSSSSSSSCKRVKLQSKVAVLIREGVSS 711

QY 140 ----- 139
DB 712 TTPAKDSSSSGLSGTGVKFSRDRSRSPFLKPDERSPAEGVKVAPGSTKPKTKAKAKAG 771

QY 140 ----- 139
DB 772 AKKAGTKGKTTPKTRKKVRSKSGSSTASGGPGSLKSKADSCSOASAKGTEETSWSGE 831

QY 140 -----PARPPP-----WTP----- 161
DB 832 ERTTKAPSTPPPKVAPPPPPALTPDSQTVDSCKTPDVSLABEASEDTGVRVGAEEEE 891

QY 162 -----PAPAPAA-----PPSTFS 173
DB 892 EEEEEEEQOATTATTTATTAAPSTAPSAGSTAGDGAEDGPAARASQLPTLPPP 948

QY 174 VVDLLYWR-----DIKKTGVFGASLFLSLTFSIVSVTAYIALALISLVTISFRIYKG 228
DB 949 -----MPWNLPAVDCTTSGV-----LALT-----ALLF----- 972

QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGH----- 267
DB 973 -----KME-----ANLASR-AKAQLIQD-TNQLRHRKPPSTLGVTPAPVPTSGFLP 1019

QY 268 -----VNC-----TIKELRLEFLVDLLV 285
DB 1020 PAPSSYLLPGSLPIGCGSGTPTPTGLVPASDKREGSSSSSEGRGDTDKYLKHLHTQERAV 1079

QY 286 DSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSFVPIYERHQAQIDHYLGLANKNVKDA 345
DB 1080 BEVK-----LSIKPYQKKDITKEEY-----KDI 1103

QY 346 WAKIOAKI----- 353
DB 1104 LRKAVHKICHKSGEINPVKSNLVAVQRYVRYFRKHGKPGDPPGPPRPKPGPPDK 1163

QY 354 --PGL 356
DB 1164 GGPGL 1168

RESULT 8
S24407
formin isoform IV - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S24407
R:Jackson-Grusby, L.; Kuo, A.; Leder, P.
Genes Dev. 6, 29-37, 1992
A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb define
A:Reference number: S24407; MUID:92112033; PMID:1339380
A:Accession: S24407
A:Molecule type: mRNA

A:Residues: 1-1206 <JAC>
A:Cross-references: UNIPROT:Q05859; EMBL:X62379; NID:g51552; PIDN:CAA4244.1; PID:g51553

Query Match 14.4%; Score 266; DB 2; Length 1206;
Best Local Similarity 17.3%; Pred. No. 1.7;
Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;

QY 5 DQSLVSSDSPPR-----PQAFKQVFRPEDEEE-----EEEE 41
DB 459 DQSPTQDDRTGRLQAVVPPPKTK-----DTEKVLKYTEAEYQAAAILHLKREHK 510
QY 42 EDEE-----DEDLEEL-EVLERK----- 58
DB 511 EEIETLQAOELKTFHIRGEHALVTARLEAEIENLKOQLEKREGCEMRDVCISTDDDC 570
QY 59 -PAA----- 61
DB 571 SPKAFRNVCITQDRETFKPCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIAHPFQT 630
QY 62 --GLSA-----APVETAPAGAPLMDFGNDFVPPAP-----RGPLPAAPPVAPERQ 105
DB 631 REGTSSSSQOKISPPAP-FTPPPLPPPL-----IPPPPLPPGLGLPPAPPPIPP--- 679
QY 106 PSWDPSVSTVPAPSPLSAAAAPSCLPEDDEPPARPPPPPA-----SVSPQAE 157
DB 680 ----VCVPSPPPPPPP-----PPTVPSPDGPPPPPPPPPLPNVLPALPNSGGPPPP 729
QY 158 VMTPPAP--APAAPSTSV-----VDLLYMRDIKKTGVVFGASLF 195
DB 730 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 776
QY 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHP-----FRAY 245
DB 777 -----IQINDKSQDAAPTLDWDSLEEPHIRT 802
QY 246 LESEVAISEELVQ-----KYSNSA---LGHVNCITKELAR 277
DB 803 SEFEYLFSDTTOQKKKPLSEAYEKNKVKYKIIKLDGKRSQTVGLISLHLEMDIQ 862
QY 278 -LFLVDLVDLSLKFAVLMVFTVVGALFNGLTLILALISLSVPVYIYERHOAIDHYLG 336
DB 863 AIFTVD-----SVVDLETALAE----- 882
QY 337 LANKNVKDMAKIQ-----AKIPGLKRAE 361
DB 883 --NRAQDELTKIRKYETSKEEDLKLDPQFLHQAIPNFABRAQ 929

RESULT 9
S11515
formin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11515
R:Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb deform
A:Reference number: S11515; MUID:90363291; PMID:2392150
A:Accession: S11515
A:Molecule type: mRNA
A:Residues: 1-1468 <Woy>
A:Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

Query Match 14.4%; Score 266; DB 2; Length 1468;
Best Local Similarity 17.3%; Pred. No. 2.8;
Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;

QY 5 DQSLVSSDSPPR-----PQAFKQVFRPEDEEE-----EEEE 41
DB 685 DQSPTQDDRTGRLQAVVPPPKTK-----DTEKVLKYTEAEYQAAAILHLKREHK 736
QY 42 EDEE-----DEDLEEL-EVLERK----- 58

Db 737 EEIETLQAOELKTFHIRGEHALVTARLEAEIENLKOQLEKREGCEMRDVCISTDDDC 796
QY 59 -PAA----- 61
Db 797 SPKAFRNVCITQDRETFKPCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIAHPFQT 856
QY 62 --GLSA-----APVETAPAGAPLMDFGNDFVPPAP-----RGPLPAAPPVAPERQ 105
Db 857 REGTSSSSQOKISPPAP-FTPPPLPPPL-----IPPPPLPPGLGLPPAPPPIPP--- 905
QY 106 PSWDPSVSTVPAPSPLSAAAAPSCLPEDDEPPARPPPPPA-----SVSPQAE 157
Db 906 ----VCVPSPPPPPPP-----PPTVPSPDGPPPPPPPPPLPNVLPALPNSGGPPPP 955
QY 158 VMTPPAP--APAAPSTSV-----VDLLYMRDIKKTGVVFGASLF 195
Db 956 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 1002
QY 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHP-----FRAY 245
Db 1003 -----IQINDKSQDAAPTLDWDSLEEPHIRT 1028
QY 246 LESEVAISEELVQ-----KYSNSA---LGHVNCITKELAR 277
Db 1029 SEFEYLFSDTTOQKKKPLSEAYEKNKVKYKIIKLDGKRSQTVGLISLHLEMDIQ 1088
QY 278 -LFLVDLVDLSLKFAVLMVFTVVGALFNGLTLILALISLSVPVYIYERHOAIDHYLG 336
Db 1089 AIFTVD-----SVVDLETALAE----- 1108
QY 337 LANKNVKDMAKIQ-----AKIPGLKRAE 361
Db 1109 --NRAQDELTKIRKYETSKEEDLKLDPQFLHQAIPNFABRAQ 1155

RESULT 10
T13286
cappuccino gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13286
R:Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.
Genes Dev. 9, 2482-2494, 1995
A:Title: Cappuccino, a Drosophila maternal effect gene required for polarity of the egg
A:Reference number: T17651; MUID:96033799; PMID:7590229
A:Accession: T13286
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1058 <EMM>
A:Cross-references: UNIPROT:Q24120; EMBL:U34258; NID:g1061333; PID:g1061334; PIDN:AAC469;
C:Genetics: capu
A:Gene: capu
A:Cross-references: FlyBase:FBgn0000256

Query Match 14.3%; Score 264.1; DB 2; Length 1058;
Best Local Similarity 16.1%; Pred. No. 1.4;
Matches 118; Conservative 47; Mismatches 117; Indels 449; Gaps 27;

QY 9 LVSSSDSPPR-----PQAFKQV-----VREPEDEEEEEE----- 42
Db 398 LLSVDEPPRRSKRCVNLTELLNASEATVYENKTAGSCVKSFDTAETQTESECEGT 457
QY 43 -----EDEDELEBEVLERKPAAGLSAAPVPTAPAGAPLMDFGNDFV-PP 88
Db 458 CKQGSSTKVDNKSAGEDG-----KPHA-----VAPPPPPPPPLPA-----EVAPP 501
QY 89 ARGPLPAPPVAPERQSPSWDPSVSTVPAPSPLSAAAAPSCLPEDDEPPAR----- 142
Db 502 PPPPPPPPPPLANYGAP---PPP-----PPPPPGSGSAPP-----PPAPIEGGG 546
QY 143 -PPPPPPASVQAEPV----- 160
Db 547 IPPPPPPMSASPSKTTISAPLPDPAEGNWFHRTNTRKSAVNPPKPMRPLYWTRIVTSA 606

```
QY 161 PPAP-----APAAPPSTVVLLYWRDIKKT-----186
D 607 PAPRPPSVANSTDSSTENSGSPDEPPAANGADAPTAPATKEI-----WTIEETPLDN 662
QY 187 -----GVVF-----190
D 663 IDEFTELFSRQAIAPVSKPKELVKRAKSIKVLDPERSRNVGLIWRSLHVPSSSEIHAIV 722
QY 191 -----GASLFL-----LLSLTVFSI-----VSV 208
D 723 HDTSVSVLEALQHSNIOATELQRIKEAAGGDIPLDHPQFLDLISLMSASERISC 782
QY 209 TAYIALALLSVTSFRIYKGVIOAIO-----234
D 783 IVFOAEFESVILLFRKLTSTVLSQLSIEDLKLVSIIILTLGNYMNGNRQORQADG 842
QY 235 -----KSDEGH-----240
D 843 FNLIDILGKLKDVKSESHITLLHFIVRTVIAQRKKEGVHPIRLPIPEPADVERAAQMD 902
QY 241 -----PFRAYLSEVAISEELVQKYSNSAL 265
D 903 FEEVOQOIFDLNKKFLGCKRTTAKVLAASRPEIMEFFKSKMEEFVEGADKSMALHQS-- 960
QY 266 GHVNCTIKELRLFL-----VDDLVDLSLKFAVL 293
D 961 -----LDECRDLFLETMRPHYHSPKACTLTLAQCTPDQFFEYWTNFTNDFKDIWK-----1010
QY 294 MVFTYVVGALFNGLTLLALLLISLFSVPVIYERHQADIDHYLGLANKVYKDAWAK---IQ 350
D 1011 -----KEITSLNELL-----MKSKQAQIE-----SRNVSTKVKSGRIS 1046
QY 351 AKIPGLKRAE 361
D 1047 LKERMLMRRSK 1057

RESULT 11
T39236
Hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39236
R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T39236
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1611 <MUR>
A:Cross-references: UNIPROT:O42854; EMBL:AL021813; PIDN:CAAL6991.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.17
A:Map position: 1

Query Match 14.2%; Score 262.4; DB 2; Length 1611;
Best Local Similarity 9.8%; Pred. No. 4.6;
Matches 127; Conservative 57; Mismatches 112; Indels 1006; Gaps 29;

QY 2 EDL-----DOSPLV-----SSSDGPPRP-----19
D 299 EELSKSRVAKDDPPVSVNTANSDEPSSSKPAKELTDLNRASFQRLNLDQKPKKSOQ 358
QY 20 -----OPAKYQFVREPDDEE-----EEEEEEDEEDL 49
D 359 EISEQEDEYDAAESDEMHSPTSTHEPESEPDQDEPSEKDKDENKDEVEEQEQQEQQI 418
QY 50 EEL-----VLERKPAAG-----62
D 419 DPEEKRIALRERMAKSGGIGMHVFLGLAIPIGKNTLRTPAKSSEAKSTTNDSS 478
```

Qy	293	-----LMMVFTYVG---ALFNGLT-----	308
Db	554	KSSNILLENNFHALVSDFLGAKLALDCNTHITTRVMGTFCGYMAPEYASSGKLTTEKSDVFS	613
Qy	309	--LILIALIS-----LFSPVPVIYERHQAOIDHYLG-----	336
Db	614	FGVLLELITGRKVDASQPLGDSELSVEWARPLLNSATETEETALADPKLRNYGVGM	673
Qy	337	-----LANKNVKDAM-----AKIOAKIPGL	356
Db	674	FRMIEAAAACIRHSATKRPMSQIVRAPDSLAEEDLTNGMLGESETINSQAQSAAEIRLP	733
Qy	357	KRKA 360	
Db	734	RRMA 737	
 RESULT 13			
A59295			
unconventional myosin-15 - mouse			
C:Species: Mus musculus (house mouse)			
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004			
C:Accession: A59295			
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mi-			
an, T.B.; Fridell, R.A.			
Genomics 61, 243-258, 1999			
A>Title: Characterization of the human and mouse unconventional myosin XV genes responsib			
A:Reference number: A59266; MUID:20021762; PMID:10552926			
A:Accession: A59295			
A>Status: preliminary; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-3511 <LIA>			
A:Cross-references: UNIPROT:O9QZ4; GB:AF144095; NID:g6224684; PIDN:AAF05904.1; PID:g6222			
C:Genetics:			
A:Gene: MGI:Myo15			
A:Cross-references: MGI:1261811			
A:Map position: 11:33.9			
F:1209-1871/Domain: myosin motor domain homology <MMO>			
 Query Match 13.9%; Score 257.1; DB 2; Length 3511;			
Best Local Similarity 9.5%; Pred.No. 50;			
Matches 136; Conservative 46; Mismatches 113; Indels 1139; Gaps 35;			
Qy	16	PGRP-----QPAFKYQFV-----REPEDEEEE-----	37
Db	388	PGMPYVYPEEPAYPWPPPIPSHPNPYAHMPMDIAELEPEETGEEROSTSRFLPSAA	447
Qy	38	-----EEEEEE 43	
Db	448	FPEQQMDKPARKSLIRKRLFRPQVKLVFGKEKLEVLPLPSLDIPLPLGDAEGSEE	507
Qy	44	DEDEDLEEVLERKPAAGLSAAPVTAP-----AAGAPL-MDF 81	
Db	508	EE-----MPPVPTMTPTHTPYMSFLTQRQNLRALSFAFGARQGLGF	548
Qy	82	GNDVFPPAPR-----GLPL-----AAPVA-----	101
Db	549	GPEGHPTPRPATSLARFLKTLSEKKPIRLRGOKARGRPVREAAYRRFGYKLGM	608
Qy	102	-PER-----QSWDPSP-----VSSTVPAPSPLSAAAVS	129
Db	609	DPDAPNTPIVLRSSQPARNNNNSHGPSRPRAPRALTHWSALISPPMPAPSPASPPLT	668
Qy	130	-----	129
Db	669	PPFGPTFSRPPRLASPYGSLRHQPWPWAAPAHVFPFPQANWMGFABPPGTSPEVAPDLA	728
Qy	130	-----	129
Db	729	FPVPRPSPFRSGRSRRRAAYGPSPSLIGSRRRPHLPSPQPSLRSLPGQGYHSPGLPSP	788
Qy	130	-----	129

Db 789 QLSLRGPPQPPPPRRRPSQLREAFSLRRASGLRPPSPVLGSPRPPSPPLLKHP 848
QY 130 -----PSKPED-----DEPPAR-----PPPP----- 146
Db 849 RHRSNLPSRLPRTWRRLSEPTTRAVKPVWHRAYPPPSAGPWGASTGALEQENQRBAE 908
QY 147 -----PPA----- 153
Db 909 DSETPTWVPLAPSMDVMDPPTQRPSPWPPEGISLGRSPPPVPENPLLEHTSPSCPEP 968
QY 154 QAE----- 156
Db 969 QSEDRVSNLTGIFLGHGHDGPGQLTKSADPSLEKPEEVVTLGDPQPAEPALNPTPPN 1028
QY 157 -----PVM----- 159
Db 1029 KVVSEKVLRLSASVPLVTCQARATWQWRHWKTVSRTPAPLAPTRAPGPLLKAGSQP 1088
QY 160 -----TPPAPAPAP----- 170
Db 1089 RAEPGRFAVMPQVRGVSSFRPKGPAPVQPPPEHPDQDPQGPAPQACSLRWFCLWPPTDA 1148
QY 171 -----STSV 174
Db 1149 HCLWSRIITYSSQSHLRGHGCHKSLMKKTRPQSQWQNKWHSIRNLPSMRSEQRHEDGV 1208
QY 175 VLLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVYATIALALLSVTISPRIYKGVIAIQ 234
Db 1209 EMTQLEDQETVL--ANL-----KTRERNLIYYIGSILSV----- 1246
QY 235 KSDEGHPFRAYLESEVAISEELVQYSNALS----- 266
Db 1247 -----NPYRMF-----AIYGEVQVQYSGRALGPNPHLFAIANLAFAKMLDAKQNCVVI 1297
QY 267 ----- 266
Db 1298 SGESGKTEATKLIRCLAMNQRDRVMQIKILEATPLLEAFGNAKTVRNDNSSRFK 1357
QY 267 -----HV----- 268
Db 1358 FVEIFLEGVICAITSYLLBKSRIVFOAKNERNHYFIYELLAGLPAQLROAFLQEA 1417
QY 269 -----NCTI-----KELRLIF----- 279
Db 1418 TYVYLNQGNCSIAKSDADDPRLLAAEMVLGFTSDQDSIFRILLASILHLGNVVFEGH 1477
QY 280 -----LVD--D 283
Db 1478 ETDAQEVAWSGAREIQAVAELOVSPGELQKAITFKVTETIREKIFTPLTVESAVDARD 1537
QY 284 LVDSLKFVLM--WVFTYVGCAL-----FNGLLTLLI-----ALI 315
Db 1538 ATAKVLIALFWLITRVNALVSPKQDTLSIALDIYGFEDLSFNSPEQLCINYANENLQ 1597
QY 316 SLFSVPVIYERHAQ----- 330
Db 1598 YLFN-KIVFQEEQEEVIREQMDWEIAPADNPQCINLISLKPVGILRLDDQCCFPQATD 1656
QY 331 -----IDHYLGLANKV-----KDM----- 346
Db 1657 HTFLQKHYHGANPLYSKPMPLPEFTIKHYAGKVTYQVHKFLDKNHQVQRQVLDLDFV 1716
QY 347 -----AKIQAKIPGLKRAE 361
Db 1717 HSRTRVVAHLFSSHAAQATAPPLRGKSSSITRLYKAHTVAAKTQSSLLDLVEKWE 1770

RESULT 14

T31065

diaphanous protein homolog p140mDia - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T31065

R:Watanabe, N.; Madaule, P.; Reid, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, Y.
EMBO J. 16, 3044-3056, 1997
A:Title: p140mDia, a mammalian homolog of Drosophila diaphanous, is a target protein for
A:Reference number: Z20961; MUID:97357293; PMID:9214622
A:Accession: T31065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1255 <WAT>
A:Cross-references: UNIPROT:O08808; EMBL:U96963; NID:G2114472; PID:G2114473; PIDN:AAC532E
A:Note: binds to GTP-bound form of Rho and binds to profilin

Query Match 13.9% Score 256.5; DB 2; Length 1255;
Best Local Similarity 14.7%; Pred. No. 3.9;
Matches 130; Conservative 42; Mismatches 135; Indels 575; Gaps 31;
QY 6 QSLVSSSDSPRPQ-----PAF----- 23
Db 406 QHLLVRNDYEARPOYYKLIBECVSQIVLHKNGTDPDKRHLQIDIERLVDQMDTKVK 465
QY 24 -----KYQFVREP 31
Db 466 EKSEAKATELEKCLDSELTARHELOVEMKMKENDPEQKLQDLQGEKDALDSEKQITAK 525
QY 32 EDEEE-----BEEDEDEDELELEVLERKPAAGLSAAPVPTAPAGAPLMDF 81
Db 526 ODLEAEVSKLTGEVAKLSKELEDKAKNEMASLAVVAVPSVSSAAVPPAPPLPG---DS 581
QY 82 GNDFPVAPRGLPA-----APPVAP----- 102
Db 582 GTVIPPPIPPPPPLPGVVPSPPLPGTCIPPPPLPGACIPPPPLPGSAAIPPPPL 641
QY 103 ---ERQPSWDSPSVSTVPAPSPISAAAASPSKLPEDDEPPARP----- 143
Db 642 PCVASIPPPPLPGATAIPPPPLPGATAIP-----PPPLPGTGIPPPPLPGSV 694
QY 144 ---PPPPASVSQAPBPVWTPPAPAPAP-----PSTSVV----- 175
Db 695 GVPPPPPLPGGGLPP---PPPPFGAPGIPPPPGMGVPPPPPPFGVGAAPVLPFGIT 751
QY 176 -----DL---LYWRDIK----- 184
Db 752 PKVYKPEVQLRRPNWSKFVAEDLSQDCFWTVKEDRFENNELFAKLTLAFSAQTSKA 811
QY 185 -----KT----- 186
Db 812 KKDQGGEEKSVQKKVKELKVLDSKTAQNLSIFLGSFRMPYQEIKNVILEVNEAVLTE 871
QY 187 -----GVVFG-----ASLFLLSLT 201
Db 872 SMIQNLIKQMPPEQKMLSELKEEYDDLAESEQFGVVMGTVPRLRPRLNAILFKL----- 927
QY 202 VFS-----IVSVTA-----VIALALL-----SVTISF- 223
Db 928 QFSEQVENIKPEIVSVTAACEELRKSENFSLSLETLVGNVYNAGSRNAGAFGNISPL 987
QY 224 ---RIYKGVIAI-----QKSDGHP-----FRAYLESEVAISEELVOK----- 259
Db 988 CKLRDTKSADQKMTLLHFLAELCENDHPEVLKFPDELAAHVEKASRVSANLQSLDOMKK 1047
QY 260 -----YNSALGHVN---CTIKEL----- 275
Db 1048 QIADVERDVQNPAAATDEKDFEVEKTSFVKDAQEQYNKLRMMHNMETLYKELGDFYVF 1107
QY 276 -----RRLFL----- 280
Db 1108 DPKLUSVEEFFMDLHNFNMFLQAVKENQKRETEKRRAKLAKEAKEKELEKQKKE 1167
QY 281 -----VDDLVDLSKFVLMVWVFTYVGALFNGLTLLILALISLFSVPVIYER 326
Db 1168 QLIDMNAEGDETVGVDMSLLEALQ-----SCAAFR-----RKR 1199
QY 327 HQAQIDHYLG-----LANKVVK-DAMAKIQAKIPGLKRAE 361
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

Db	1200	GPRQVNRKACAVTSLASELTAKDDAMAPGVKVP---KKSE	1238
RESULT 15			
A59266			
unconventional myosin-15 - human			
C:Species: Homo sapiens (man)			
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004			
C:Accession: A59266			
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mian, T.B.; Fridelli, R.A.			
Genomics 61, 243-258, 1999			
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsible for non-syndromic deafness			
A:Reference number: A59266; MUID:20021762; PMID:10552926			
A:Status: preliminary; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-3530 <LIA>			
A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PIDN:AAF05903.1; PID:g6224682			
F:1225-1887/Domain: myosin motor domain homology <NMO>			
Query Match 13.8%; Score 255.5; DB 2; Length 3530;			
Best Local Similarity 9.9%; Pred. No. 57;			
Matches 140; Conservative 41; Mismatches 125; Indels 1105; Gaps 36;			
QY	16	PPRQPAFKYQF-----VREPEDEEE-----EE-----	41
Db	416	PTTSPHNHYAMDDIAELEPEDEGVERQGTFRLPAAFFEQGMDKPARSKLSLR	475
QY	42	-----EEDEDELEL-----	52
Db	476	KFLPRPQVKLFGKLEVLPLPPSLDPLPLGDADEEDEELPPVSAVYGHFWGFL	535
QY	53	-----EVLKPKAAGLS-----	64
Db	536	TPQRNLQRALSAGAHGILGFCGRPVPRPATSILARLKKTLSEKPIARLGSQKT	595
QY	65	-----	64
Db	596	RAGGPAVREAAKYRFGYKLAGMDPEKPGTIVLRRAPRARSSNDARRPPAPQAPRTLS	655
QY	65	-----AAP--VPTAPA 73	
Db	656	HMSALLSPVPPRPPSSGPPAPPPLSGLPSPASPGSLRRHPPPPWAAAPAHVPPAQ	715
QY	74	AG-----APLMD 80	
Db	716	ASGWAFFEPVAVSPEVPPDLLAFPPRPSFRGSRERRGAAFGFGASPRASRRRAWSPLAS	775
QY	81	-----FGNDFVPPA-----	89
Db	776	PQSLRSSPGLGYCSPPLAPSPQLSLRTGTFPPFLPPARRPRSLQSPAPRAAGRLGP	835
QY	90	-----PRGLPAAPPV-----	100
Db	836	PGSPLGSPRPPSPPLGLCHSPRRSLNLSRPLHTWRRLSEPPTRAVKPVQLPFRPP	895
QY	101	-----APERQPSWD-----	109
Db	896	RAGWAPLEHRSREPEDESETPTWTVPLAPSDVDMPTQRPSPFWPGAGSRGRFSR	955
QY	110	PSVSVTV-----PAPSP-----	132
Db	956	PPVPENPFLLQLGVPSPPLQPEDPAADMTRVFLGRHHPGPGQLTKSAGPTPEKPEEB	1015
QY	133	-----LPEDDEPPARPP-----	145
Db	1016	ATLGDPLPAETKEPTPAPPKDVTPPKDITPPKDVLPQKTLRPSLSYPLAACDQTRATW	1075
QY	146	PP-----PASV 151	
Db	1076	PMWRHGTLPOAAAPLAPTRAPEPLPKGERRQAAPGRFAVVMRVQKLSSFORVGPATL	1135

QY	152	SPOAEPVWTP-----PAP-----APAA-----	168
Db	1136	KPQVQPIQDPKPRACSLRWSCLWLADAYCPWVRVHTHPQSCHLGPAAACLSLRGSWEV	1195
QY	169	-PPS-----TSVVDLLYMRDIKKTGVVFGASLPLLLSLTVFSI	205
Db	1196	GPPSWKMKHSIRNLSPMPRECHGEDGVEDMTQLEDLOET-----TVLSN	1241
QY	206	VSVT-----AYIALALLSVT--ISFRIYKGVIAIQKSDGHPFRAYLESEVAISEEL	256
Db	1242	LKIRFERNLITYTIGSILSVNPNYQMGIV-----GPEQ	1275
QY	257	VQKYSNSALG-----	266
Db	1276	VOQYNGRAGLGNPPHPLFAVANLAFAKMLDAKQNCIIISGESGSGKTEATKLIRLYLAM	1335
QY	267	-----	266
Db	1336	NQKREVMQIKILEATPLLESFGNAKTVRDNNSSRFKPVETFLGGVIGSAITSQYLLE	1395
QY	267	-----HV-----NCTI-----KEL	275
Db	1396	KSRIVFOAKNERNYHIFYELLAGLPAQLRQAFSLQEAETVYVYLNQGNCEIAGKSDADF	1455
QY	276	RRLF-----	279
Db	1456	RLLAAMEVLGFSSEDDQSIFRILASILHLGNVYFEKYETDAQEVASVVSAREIQVAEL	1515
QY	280	-----LVD--DLVDSLKFAVLM-WVFTYVYCAL--	303
Db	1516	LQISPEGLQKAITFKVTETMREKIPTPLTVESNVDARDAIAKLYIALLPSWLITRVNALV	1575
QY	304	-----FNLTLIL-----ALISLFSVPVIYERHQ-----AQID--	332
Db	1576	SPRODTLSIALLDIYGFEDLSFNSPEQLCINVANENLQVLFNKIVFOEEQEEVIREQIDW	1635
QY	333	-----	332
Db	1636	QBITPADNOPRINLISLKPYGILRLDDQCCFPQATDHTFLQKCHYHGHGANPLYSKPMP	1695
QY	333	-----HYLGLANKV-----KDM-----	346
Db	1696	LPEFTIKHYAGKTVYQVHKFELDKNHDQVQDVLDFVRSTRVRVAHLFSSHAPQAAPQL	1755
QY	347	-----AKIQAKIPGLKRAE 361	
Db	1756	GKSSSVTRLYKAHTVAAKQQSILLIVERKE 1786	

Search completed: June 23, 2005, 10:57:02
Job time : 33.0347 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 10:17:56 ; Search time 114.158 Seconds
(without alignments)
1619.338 Million cell updates/sec

Title: US-09-830-972-29-FUSED

Perfect score: 1850

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIOAKIPGLKRAE 361

Scoring table: BLOSUMP2
Gapop 10.0 , Gapext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1933.9	99.1	392	2	Q96B16	Q96B16 homo sapien
2	1756.9	95.0	1192	1	RTN4 HUMAN	Q9ncq3 homo sapien
3	1669.8	90.3	343	2	Q61PNO	Q61pno homo sapien
4	1533	82.9	375	2	Q8BHF5	Q8bhf5 mus musculus
5	1523.1	82.3	356	2	Q8BH78	Q8bh78 mus musculus
6	1513	81.8	357	2	Q8K3G7	Q8k3g7 mus musculus
7	1478.8	79.9	1163	1	RTN4_RAT	Q9jkl1 rattus norv
8	1455.3	78.7	1162	2	Q8BGM9	Q8bgm9 mus musculus
9	1441.2	77.9	1163	2	Q8K3G8	Q8k3g8 mus musculus
10	1028	55.6	986	2	Q8IU44	Q8iu44 homo sapien
11	994	53.7	1046	2	Q8BCK7	Q8bck7 mus musculus
12	989.2	53.5	639	2	Q8K290	Q8k290 mus musculus
13	986.8	53.3	578	2	Q8QW95	Q8qw95 mus musculus
14	974.6	52.7	658	2	Q6RS58	Q6rs58 gallus gall
15	927	50.1	199	2	Q7YRW9	Q7yrw9 bos taurus
16	923	49.9	199	2	Q6IM70	Q6im70 sus scrofa
17	919	49.7	187	2	Q6IG15	Q6ig15 sus scrofa
18	918	49.6	199	2	Q7PCJ7	Q7pcj7 macaca fasc
19	914.5	49.4	1024	2	Q6JRV2	Q6jrv2 xenopus lae
20	912.6	49.3	1043	2	Q6JRV0	Q6jrv0 xenopus lae
21	912.4	49.3	1055	2	Q6JRV1	Q6jrv1 xenopus lae
22	911	49.2	199	1	RTN4 MOUSE	Q99p72 mus musculus
23	903.8	48.9	315	2	Q6IFV4	Q6ifv4 xenopus tro
24	900.5	48.7	330	2	Q6JRV4	Q6jrv4 xenopus lae
25	897.2	48.5	311	2	Q6JRV3	Q6jrv3 xenopus lae
26	886.4	47.9	1013	2	Q6JRV9	Q6jrv9 xenopus lae
27	884.5	47.8	1032	2	Q6JRV7	Q6jrv7 xenopus lae
28	883.3	47.7	1044	2	Q6JRV8	Q6jrv8 xenopus lae
29	883.2	47.7	199	2	Q7T224	Q7t224 gallus gall
30	881.2	47.6	323	2	Q6JRW1	Q6jrw1 xenopus lae
31	878.9	47.5	304	2	Q6JRW0	Q6jrw0 xenopus lae

RESULT 1

Q96B16	ID	Q96B16	PRELIMINARY;	PRT;	392 AA.
AC	Q96B16;				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Reticulon 4, isoform D (RTN4 isoform B2).				
GN	Name=RTN4;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RA	Strausberg R.;				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;				
RA	Oertle T., Huber C., van der Putten H., Schwab M.E.;				
RT	"Genomic structure and functional characterisation of the promoters of				
RT	human and mouse nogo/rttn4."				
RL	J. Mol. Biol. 325:299-323(2003).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Van der Putten H.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC016165; AAH16165.1; -.				

Q6jrw2 xenopus lae
Q9gm33 macaca fasc
Q8k0t0 mus musculus
Q16799 homo sapien
Q8k4s4 mus musculus
Q64548 rattus norv
Q90638 gallus gall
Q6ifv5 xenopus tro
Q6jrv6 xenopus lae
Q6pb23 xenopus lae
Q6jrw4 xenopus lae
Q6jrw3 xenopus lae
Q7t222 carassius a
Q6ie16 cyprinus ca

Qy	172	-----	171
Db	661	EAAMSVLSLKVGSGIKEEIKBPENINAALQETAPYISIACDLIKETKLSAEPADPDSYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPHSELVSDSSPDSEPDVLFSDSDIPDVQKQDETVMLVKESLTETSPFMSI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFTSDSSPIEIIDFPTLLISSKTDSPFKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEKISFSDDDPSKNGSATSKVLLLPDVSALAT	960
Qy	172	-----	189
Db	961	QAEIESIVKPKVLKVEAKKLPSDTEKEDRSPSAFSAELSKTSVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCITKEIRLFLVDDLVDSLKFAVLMWVFTYVGFALFNGLTLL	309
Db	1081	VAISEELVQKYSNSALGHVNCITKEIRLFLVDDLVDSLKFAVLMWVFTYVGFALFNGLTLL	1140
Qy	310	LILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE	361
Db	1141	LILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE	1192
RESULT 3			
Q6IPNO			
ID	Q6IPNO	PRELIMINARY;	PRT; 343 AA.
AC	Q6IPNO		
DT	05-JUL-2004	(TREMBlrel. 27, Created)	
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)	
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)	
DE	RTN4	protein.	
GN	Name=RTN4;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUB=Eye;		
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,		
RA	Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.B.,		
RA	Jones S.J., Marra M.A.;		
RT	"generation and initial analysis of more than 15,000 full-length human		
RT	"and mouse cDNA sequences."		

RL	Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903(2002).
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Eye;	
RA	Strausberg R.;	
RL	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; BC071848; AAH71848.1; -.	
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.	
DR	InterPro; IPR003386; Reticulon.	
DR	Pfam; PF02453; Reticulon; 1.	
DR	PROSITE; PS00845; RETICULON; 1.	
SR	SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;	
	Query Match	90.3%; Score 1669.8; DB 2; Length 343;
	Best Local Similarity	96.2%; Pred. No. 2.2e-46;
	Matches 329; Conservative	0; Mismatches 1; Indels 12; Gaps 1
Qy	32	EDDEEEEDDEDEDELEVLERKPAAGLSAAPVTPAAAGAPLMDFGNDVFVPAPR 91
Dd	2	EDDEEEEDDEDELEVLERKPAAGLSAAPVTPAAAGAPLMDFGNDVFVPAPR 61
Qy	92	GPIPAAPVPAPEQPSPDPSVSTVPAPPLSAAAVSPSKLPDDDEPPARPAPPPASV 151
Dd	62	GPIPAAPVPAPEQPSPDPSVSTVPAPPLSAAAVSPSKLPDDDEPPARPAPPPASV 121
Qy	152	SPOAPEVWTPPAPAPAPPSTS-----VDLLYWRDIKKTGWVGASLFLLLS 199
Dd	122	SPOAPEVWTPPAPAPAPPSTPAAPKRGGSGSVVDLLYWRDIKKTGWVGASLFLLLS 181
Qy	200	LTVFSIVSTAYIALALLSVTISPRIYKGVIQAIOKSDGEHPFRAYLESEVAISEELVOK 259
Dd	182	LTVFSIVSTAYIALALLSVTISPRIYKGVIQAIOKSDGEHPFRAYLESEVAISEELVOK 241
Qy	260	YSNSALGHVNCTIKELRRFLVDLDLSLFAVMVFTTYGALFNGTLILALISLFS 319
Dd	242	YSNSALGHVNCTIKELRRFLVDLDLSLFAVMVFTTYGALFNGTLILALISLFS 301
Qy	320	VPVIYERHQAIIDHYLGANKNVKDAMAKIQAKIPGLKRKA 361
Dd	302	VPVIYERHQAIIDHYLGANKNVKDAMAKIQAKIPGLKRKA 343
RESULT 4		
QBHHFS	PRELIMINARY;	PRT; 375 AA.
ID	QBHHFS	
AC	QBHHFS;	(TrEMBLrel. 23, Created)
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE	RTN4.	
GN	Name=Rtn4;	
OS	Mus musculus (Mouse);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129/SvcJ7; and 129SvcJ7;	
RX	MEDLINE=42376540; PubMed=12486097; DOI=10.1016/S0022-2836(02)01179-8;	
RT	Oertle T., Huber C., van der Putten H., Schwab M.B.;	
RT	"Genomic structure and functional characterisation of the promoters of	
RT	human and mouse nogo/rtn4.";	
RL	J. Mol. Biol. 325:299-323(2003).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129/SvcJ7;	
RA	Van der Putten H.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=129SvcJ7;	
RA	Van der Putten H., Mir A.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	

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DR EMBL; AY102282; AAM73504.1; -.
DR EMBL; AY102286; AAM73509.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005155; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BB671AE6 CRC64;

Query Match      82.9%; Score 1533; DB 2; Length 375;
Best Local Similarity 82.8%; Pred. No. 7.4e-42;
Matches 317; Conservative 13; Mismatches 23; Indels 30; Gaps 7;

QY 1 MEDLQSPVLSS--DSPRRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 59
DB 1 MEDIDQSSLVSSADSPRRPQPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDELEVLKRP 60

QY 60 AAGLSAAPTAPAGAPLMDGNDVPPAPRGPLPAAPVAPRQPSWDPSVSTVPA 119
DB 61 AAGLSAAPTAP--PAA-APLDFSSDVPAPRGPLPAAPTAPRQPSWERSPAAS--A 114

QY 120 PSLPLSAAVPSKLPEDDEPPAPPPPPASVSPQAEPTVTPA----- 165
DB 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAEPPSTPAAPKRRGSGVDL 172

QY 166 ---PAAP-----PSTVVDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAYIALALLS 218
DB 173 PALPASEPVISSAVVDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAYIALALLS 232

QY 219 VTISPRIYKGVIAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITIKELRL 278
DB 233 VTISPRIYKGVIAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITIKELRL 292

QY 279 FLVDDLVDLSKFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIA 338
DB 293 FLVDDLVDLSKFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIA 352

QY 339 NKNVKDAMAKIQAKIPGLKRAE 361
DB 353 NKSVDKAMAKIQAKIPGLKRAE 375

RESULT 5
OB8H78 PRELIMINARY; PRT; 356 AA.
AC OB8H78;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVCJ7; and 129SVCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVCJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102281; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005155; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match      82.3%; Score 1523.1; DB 2; Length 356;
Best Local Similarity 84.5%; Pred. No. 1.4e-41;
Matches 315; Conservative 11; Mismatches 18; Indels 29; Gaps 7;

QY 1 MEDLQSPVLSS--DSPRRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDELEVLKRP 59
DB 1 MEDIDQSSLVSSADSPRRPQPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDELEVLKRP 60

QY 60 AAGLSAAPTAPAGAPLMDGNDVPPAPRGPLPAAPVAPRQPSWDPSVSTVPA 119
DB 61 AAGLSAAPTAP--PAA-APLDFSSDVPAPRGPLPAAPTAPRQPSWERSPAAS--A 114

QY 120 PSLPLSAAVPSKLPEDDEPPAPPPPPASVSPQAEPTVTPA----- 173
DB 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPSTPAAPKRR 163

QY 174 -----VDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYK 228
DB 164 GSGSVVDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYK 223

QY 229 VIQATQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITIKELRLFLVDDLVDLSL 288
DB 224 VIQATQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNCITIKELRLFLVDDLVDLSL 283

QY 289 KFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIANKNVKDAMAK 348
DB 284 KFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIANKNVKDAMAK 343

QY 349 IQAKIPGLKRAE 361
DB 344 IQAKIPGLKRAE 356

RESULT 6
OB8H78 PRELIMINARY; PRT; 357 AA.
AC OB8H78;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nogo-B.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Jin W., Li R., Long M., Shen J., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114153; AAM77069.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
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FT CONFLICT 1130 1131 Missing (in Ref. 3: AAD31020).
SQ SEQUENCE 1163 AA; 126386 MW; 8CB94B09E94F086 CRC64;

Query Match
Best Local Similarity 79.9%; Score 1478.8; DB 1; Length 1163;
Matches 320; Conservative 11; Mismatches 25; Indels 812; Gaps 7;

QY 1 MEDLQSPVSSS-DSPRPQPAFKYQFVREDEDE-EEEEEEDEDEDEDELEVLK 58
DB 1 MEDIQSSLVSSSTSPRPAPFAKYQFVTEPEDEDEDEDEDEDEDEDEDELEVLK 60

QY 59 PAAGLSAAVPPTAPAGALMDFGNDVPPAPRGPLPAPAPVAPRQPSWDSSTVP 118
DB 61 PAAGLSAAVP--PAAALPDLFSSDVPPAPRGPLPAPAPVAPRQPSWERSPAA---P 115

QY 119 APSPLSAAVSPKLPEDDEPPAPPPPPASVPOAEFVWTPPAPA----- 165
DB 116 AFSPLPAAAVLSPKLPEDDEPPAPPPPPAGASPLAEPAPAPSTPAAPKRRGSGVDST 175

QY 166 ----PAA----- 168
DB 176 LPALPAASEPVPISSAEKIMDLMEQGNVSSGQEDFPSVLLETAASPLSPLSTVSPK 235

QY 169 ----- 168
DB 236 EHYGLNLSAVSSSEGTIBETLNEASKELPERATNPFVNRDLAPSELSYSEMGSSFKGS 295

QY 169 ----- 168
DB 296 PKGESAILVENTKEEVIVRSKEDLVCSAALHSPOESPVGKEDRVSPKTDIFNEMQ 355

QY 169 ----- 168
DB 356 MSVAPVRBEYADFKPQEAWEKDTYEGSRDVLAAARANVESKVRDKCLEDSLEQKSLG 415

QY 169 ----- 168
DB 416 DSEGRNEDASPTPEPVKDSRAYITCASFTSATESSTANTPPLLEDHTSNTKDEK 475

QY 169 ----- 168
DB 476 BERKAQIITEKTSPTKSNPLVAVQDSEADYVTTDLTSKVTEAANVMPEGLTPDLVQEA 535

QY 169 ----- 168
DB 536 CESELNEATGTKIAYETKVDLVQTSBAIQESLYPTAQLCPSPPEAEATPSVLPDIMEA 595

QY 169 ----- 170
DB 596 PLNSLLPSAGASVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEG 655

QY 171 ----- 170
DB 656 EPESFNAAVOETEAPYISTACDLIKETKLTSTPSPDPSNYSIAKPEKSPHEALVEDS 715

QY 171 ----- 170
DB 716 SPESEPVDLFSDSIPEVPQTQBEAVMLMESLITEVSETVAQKBERLSASQELGKPYL 775

QY 171 ----- 170
DB 776 ESFQPNLHSTKDAAGNDIPTLTKEKISLQMBEFTAIYSNDLLASSKEDKIKESFTSD 835

QY 171 ----- 170
DB 836 SSPIETIDEPFTVSAKODSPKLAKETVLEVDKSEIANIOSGADSLPCLELPCLDSFK 895

QY 171 ----- 170
DB 896 NIYPKDEVHSDSEFSNRSVSKASISPSNVALEBPQTEMGSIKSVSKSLTKEAKKLPSD 955

QY 171 -----STSVDDLWYRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIA 213
DB 171 -----STSVDDLWYRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIA 213
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DB 956 TEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIA 1015
QY 214 LALLSVTTSFRIYKGVIAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCTIK 273
DB 1016 LALLSVTTSFRIYKGVIAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIK 1075
QY 274 ELRRFLVDDLVDSLKFAVLMWFTYVVGALFNGLTLLILALISLSPVPIYERHQAIQDH 333
DB 1076 ELRRFLVDDLVDSLKFAVLMWFTYVVGALFNGLTLLILALISLSPVPIYERHQVQIDH 1135
QY 334 YLGLANKVVKDAMAKIQAKIPGLKKA 361
DB 1136 YLGLANKVVKDAMAKIQAKIPGLKKA 1163

RESULT 8
Q8BGM9 PRELIMINARY; PRT; 1162 AA.
ID Q8BGM9;
AC Q8BGM9;
DT 01-MAR-2003 (TREMELrel. 23, Created).
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE RTN4.
GN Name=RTN4;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7; and 129SVCJ7;
RX MEDLINE=22376340; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102284; AAM73506.1; -
DR EMBL; AY102286; AAM73511.1; -
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
SQ SEQUENCE 1162 AA; 126612 MW; 855697PBEE11781F CRC64;

Query Match
Best Local Similarity 78.7%; Score 1455.3; DB 2; Length 1162;
Matches 319; Conservative 11; Mismatches 23; Indels 817; Gaps 8;

QY 1 MEDLQSPVSSS-DSPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLK 59
DB 1 MEDIQSSLVSSADSPPRPAPFAKYQFVTEPEDEDEDEDEDEDEDELEVLK 60

QY 60 AAGLSAAVPPTAPAGALMDFGNDVPPAPRGPLPAPAPVAPRQPSWDSSTVP 119
DB 61 AAGLSAAVP--PAA-APLDFSSDVPPAPRGPLPAPAPVAPRQPSWERSPAA---A 114

QY 120 PSPLSAAVSPKLPEDDEPPAPPPPPASVPOAEFVWTPPAPA----- 165
DB 115 PSPLPAAAVLSPKLPEDDEPPAR---PPAPAGASPLAEPAPSTPAAPKRRGSGVD 172
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QY 166 ---PAA----- 168
DB 173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSPVLPETAASLPSLSPLSTVSPKE 232
QY 169 ----- 168
DB 233 HGYLGNLSAVASTECTIBETLNEASRELPERATNPFVNRESAEFVLEYSNGSSFNQSP 292
QY 169 ----- 168
DB 293 KGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPOESPATLTKVVKEDGVMSPEKTMDF 352
QY 169 ----- 168
DB 353 NEMKMSVAVPREEYADPKPEQAEVKTDEGSRDVLAAANMESKVDKCKCFEDSLQK 412
QY 169 ----- 168
DB 413 GHGKDESENENASFPRTPELVKDGSRAYITCDSFSSATSTAAANIFPVLEDHTSENKTD 472
QY 169 ----- 168
DB 473 EKKIEERAKAIITKTSKPTSNPFLVAIHDSEADYVTTDNLSKVTEAVATMPEGLTDPDL 532
QY 169 ----- 168
DB 533 VQACESELNEATGKIAVETKVDLVQTSIAQESIIPTAQICPSFEAEATPSPVLPDI 592
QY 169 ----- 170
DB 593 VMEAPLNSLLPSTGASVAQPSASPLEVPSVSDGKLEPENPPPYEAMSVALKTSDAK 652
QY 171 ----- 170
DB 653 BEIKEPEFNAQAEAPYISACDLIKETKLTSTEPSPEFSNYSEIAKPKSVDPHCEL 712
QY 171 ----- 170
DB 713 VDDSSPEPDLFSDSDTSIPEVPQOEAEVLMKESLTVSTVQHKHKLRSASPOEV 772
QY 171 ----- 170
DB 773 GRPYLESFQPNLHITKDAASNEIPTLTKEITISLQWBEFNTAIYSDNDLLSKDKMKES 832
QY 171 ----- 170
DB 833 ETFSDSSPIIIDEPTFVSADSKPEYTDLEVSNKEIANVQSGANSLPCSELPCDLS 892
QY 171 ----- 170
DB 893 FKNTYPKDEAHVDSFKSRSSVKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLP 952
QY 171 -----STSVDDLWYRDITKKTGVFGASLFLLLSLTVPSIVSVTAY 211
DB 953 SDTEKEDSLTAVLSAELNKTSDWLLWYRDITKKTGVFGASLFLLLSLTVPSIVSVTAY 1012
QY 212 IALALLSVTISPRIYKGVIAQOKDEGHPFRAYLESEVAISEELVQKYSNLSALGHVNST 271
DB 1013 IALALLSVTISPRIYKGVIAQOKDEGHPFRAYLESEVAISEELVQKYSNLSALGHVNST 1072
QY 272 IKELRRLFLVDVLSLKFVLMWFTYVVGALFNGLTLLILALISLFSVPVYRHRQAI 331
DB 1073 IKELRRLFLVDVLSLKFVLMWFTYVVGALFNGLTLLILALISLFSVPVYRHRQAI 1132
QY 332 DHYLGLANKNVKDAKQAKIPLKRAE 361
DB 1133 DHYLGLANKNVKDAKQAKIPLKRAE 1162
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RESULT 9

Q8K3G8

ID Q8K3G8

PRELIMINARY;

PRT; 1163 AA.

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AC Q8K3G8;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Nogo-A.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Jin W., Long M., Li R., Ju G.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endorplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;
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Query Match 77.9%; Score 1441.2; DB 2; Length 1163;

Best Local Similarity 27.2%; Pred. No. 1e-37;

Matches 318; Conservative 11; Mismatches 24; Indels 818; Gaps 9;

QY 1 MEDDQSLVSS--DPPRPOPAKYQVREPEDEEEEEDEDEDEDELEVLKRP 59

DB 1 MEDDQSLVSSADSPRPAPKQYVREPEDEEEEEDEDEDEDELEVLKRP 60

QY 60 AAGLSAAVPPTAPAGAPLMDFGNDVPPAPRGPLPAPPAVPERQPSWDPSPVSTVPA 119

DB 61 AAGLSAVFPV--PAA-APLDFSSDVPAPRGPLPAPPAVPERQPSWSPASPAAS--A 114

QY 120 PSLPSSAAVSPSKLPEDDEPPAPRPSPASVQAEVPTPPAPA----- 165

DB 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAEPAAPSTPAAPKRKSGSVDEL 172

QY 166 ---PAA----- 168

DB 173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSPVLPETAASLPSLSPLSTVSPKE 232

QY 169 ----- 168

DB 233 HGYLGNLSAVASTECTIBETLNEASRELPERATNPFVNRESAEFVLEYSNGSSFNQSP 292

QY 169 ----- 168

DB 293 KGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPOESPATLTKVVKEDGVMSPEKTMDF 352

QY 169 ----- 168

DB 353 NEMKMSVAVPREEYADPKPEQAEVKTDEGSRDVLAAANMESKVDKCKCFEDSLQK 412

QY 169 ----- 168

DB 413 GHGKDESENENASFPRTPELVKDGSRAYITCDSFSSATSTAAANIFPVLEDHTSENKTD 472

QY 169 ----- 168

DB 473 EKKIEERAKAIITKTSKPTSNPFLVAIHDSEADYVTTDNLSKVTEAVATMPEGLTDPDL 532

QY 169 ----- 168

DB 533 VQACESELNEATGKIAVETKVDLVQTSIAQESIIPTAQICPSFEAEATPSPVLPDI 592

QY 169 ----- 170

DB 593 VMEAPLNSLLPSTGASVAQPSASPLEVPSVSDGKLEPENPPPYEAMSVALKTSDAK 652

QY 171 ----- 170

Db 653 BEIKPESFNAAQAEAPYISACDLIKETKLTSTPSPGFSNYSEIAKFEKSVDPHCEL 712
 QY 171 -----
 Db 713 VDDSSPESFPVDFSDSDSIPEVPOQEAAVLMKESLTVSETVTQHKHKLRSASQEV 772
 QY 171 -----
 Db 773 GKPYLESFQPNLHITKDAASNEIPLTKKETISLOWEENFTAIYNSDNDLLSKEDMKES 832
 QY 171 -----
 Db 833 ETFSDSPIETIDEPFTFVSAXDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCLDLS 892
 QY 171 -----
 Db 893 FRNTYPKDEAHVDSBFSKRSRSVSVPLLLPNVSALESQIEMGNIVKPKVLTKAEKLP 952
 QY 171 -----
 Db 953 SSTEKEDSLTAVLSAELNKTSSVDLLYWRDIKKTGVYFGASLFLLSLTTFVSIVSVA 1012
 QY 211 YIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNC 270
 Db 1013 YIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNS 1072
 QY 271 TIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNLGLTLILALISLFSVPVIERHOAQ 330
 Db 1073 TIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNLGLTLILALISLFSVPVIERHOAQ 1132
 QY 331 IDHYLGLANKNVKDAWAKIQAIPGLKRAE 361
 Db 1133 IDHYLGLANKNVKDAWAKIQAIPGLKRAE 1163

RESULT 10
 Q8IU4 PRELIMINARY; PRT; 986 AA.
 AC Q8IU44;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).
 GN Name=RTN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.";
 RL J. Mol. Biol. 325:299-323 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102285; AAM64244.1; -
 DR EMBL; AY123246; AAM64250.1; -
 DR EMBL; AY123247; AAM64251.1; -
 DR EMBL; AY123248; AAM64252.1; -
 DR EMBL; AY123249; AAM64253.1; -
 DR EMBL; AY123250; AAM64254.1; -

DR EMBL; AY123245; AAM64249.1; -
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS0845; RETICULON; 1.
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;
 Query Match 55.6%; Score 1028; DB 2; Length 986;
 Best Local Similarity 39.2%; Pred. No. 1.8e-24;
 Matches 250; Conservative 27; Mismatches 60; Indels 300; Gaps 17;
 QY 3 DLQDS-----PLVSSSDSPRRP-----Op--- 21
 Db 372 DLVQTSVWQSLPAAQLCFSESEATPSPVLPIVMEAPLNSAVSAGASVQPSSS 431
 QY 22 -----AFKIQFVR-EPED-----EE-----EEEEEEDEDELELE----- 53
 Db 432 PLEASSVNYSEIKHEPENPPPEEAMSVLKKVSGIKEEIKPENINAAALQTEAPYISI 491
 QY 54 -----VLERKPAAGLSAAPV-----TAPAGAPLMDFGNDF 85
 Db 492 ACDLIKETK-----LSAEPAPDFSDYSEMAKVQVPDHSSELVEDSSPOS-EPVDLFSDDS 546
 QY 86 VPPAP-----RGPLPAAP----- 99
 Db 547 IPDVQKQDQETVLMVKESLTETSPESMIEYENKEKLSALPPGEGKPYLESFKLSLDNTKD 606
 QY 100 -VAP-----ERQPSWDPSPV----- 113
 Db 607 TLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFTSKAQIRETETFTSDSPIEIDEPF 666
 QY 114 ----- 113
 Db 667 TLISSTDSFSKLAREYTDLEVSHKSEIANAPDAGSLPCTELPHDLSLKNQPKVEEKI 726
 QY 114 -----SSTVPAPPLSAAA-----VSP-----SKLPEDDEPPARP 144
 Db 727 SFSDDFSKNGSATSKVLLLPDVSALATQAEIESIVKPKLVKEAKKLPSTEKEDR-- 784
 QY 145 PPPASVSPQAEPPVWTPPAPAPAPSTSVVLLLYWRDIKKTGVVFGASLFLLSLTVFS 204
 Db 785 -----SPSAIFSALSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFS 829
 QY 205 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSA 264
 Db 830 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSA 889
 QY 265 LGHVNCTIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNLGLTLILALISLFSVPVIY 324
 Db 890 LGHVNCTIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNLGLTLILALISLFSVPVIY 949
 QY 325 ERHOAQIDHYLGLANKNVKDAWAKIQAIPGLKRAE 361
 Db 950 ERHOAQIDHYLGLANKNVKDAWAKIQAIPGLKRAE 986
 RESULT 11
 Q8BGK7 PRELIMINARY; PRT; 1046 AA.
 AC Q8BGK7;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE RTN4.
 GN Name=RTN4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7; and 129SvCJ7;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;

RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RC STRAIN=129/SVCJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102280; AAM73502.1; -;
DR EMBL; AY102286; AAM73507.1; -;
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IDA.
DR GO; GO:000515; P:protein binding; IPI.
DR GO; GO:000515; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 53.7%; Score 994; DB 2; Length 1046;
Best Local Similarity 38.6%; Pred. NO. 2.6e-23;
Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;

QY 3 DLQDS-----PLVSSSDSPPRP-----QPA-- 22
DB 440 DLVQTSEAIQESIVPTAQLCPSEAEATPSPVLPIVMEAPLNSLLPSTGASVAQPSAS
QY 23 -----FKYQFVR-EPDEDEEEEEE-----HEEDEDELELE----- 53
DB 500 PLEVSPSPSYDGIKLEPNPPPEEAMSVALKTSKKEIKPESEFNAAQAQEAAPYISI 559
QY 54 -----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF 85
DB 560 ACCLIKETK-----LSTEPSPEFSNYSEIAKPEKSVDPHCELVDSDSPES-EPVDFLSDDS 614
QY 86 VPPAPR-----GFLPAAAPPVAPERQPSW----- 108
DB 615 IPEVPTOEAEAVMLKESITVETVTOHKHKLRSASQEVGKPYLESFQNLHITKDA 674
QY 109 -----DFSPVSVTPAPSP 122
DB 675 ASNEIPTLTKEETISLQMEEFNTAISNDLLSSKEDKMKESITPFSPIEIIDEFPTF 734
QY 123 LSAAPVSP-----SKLPED-----DEPPARPPPPP 147
DB 735 VSAKDDSPKEYTDLVSNKSEIANVQSGANSLPCLSPCLDFKNTYKDE----- 785
QY 148 PASVSPQAPVPTPPAPAPAPS----- 171
DB 786 -AHVSDFSKSRSSSVKVPVLLPNVSALESQIEMGNIVKPKVLTKEAEKLPSTDEKDR 844
QY 172 -----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALALLSV 219
DB 845 SITAVLSAELNKTSTVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSTAYIALALLSV 904
QY 220 TISPIYKGVIOAIQKSDGHPFRAYLSEVAISELVQKYSNLSALGHVNCITKELRLF 279
DB 905 TISPIYKGVIOAIQKSDGHPFRAYLSEVAISELVQKYSNLSALGHVNCITKELRLF 964
QY 280 LVDDLVDLSLKFVLMWFTYVVGALFNGLTLILALISLFSVPVIYERHQAQIDHYGLAN 339
DB 965 LVDDLVDLSLKFVLMWFTYVVGALFNGLTLILALISLFSVPVIYERHQAQIDHYGLAN 1024
QY 340 KVVKQAMAKIQAKIPLKRAE 361
DB 1025 KVVKQAMAKIQAKIPLKRAE 1046

RESULT 12
Q8K290 PRELIMINARY; PRT; 639 AA.
ID Q8K290
AC Q8K290;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name-Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032192; AAH32192.1; -;
DR MGD; MGI:1915835; Rtn4
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 53.5%; Score 989.2; DB 2; Length 639;
Best Local Similarity 38.6%; Pred. NO. 1.2e-23;
Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;

QY 3 DLQDS-----PLVSSSDSPPRP-----QPA-- 22
DB 33 DLVQTSEAIQESIVPTAQLCPSEAEATPSPVLPIVMEAPLNSLLPSTGASVAQPSAS 92
QY 23 -----FKYQFVR-EPDEDEEEEEE-----HEEDEDELELE----- 53
DB 93 PLEVSPSPSYDGIKLEPNPPPEEAMSVALKTSKKEIKPESEFNAAQAQEAAPYISI 152
QY 54 -----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF 85
DB 153 ACCLIKETK-----LSTEPSPEFSNYSEIAKPEKSVDPHCELVDSDSPES-EPVDFLSDDS 207
QY 86 VPPAPR-----GFLPAAAPPVAPERQPSW----- 108
DB 208 IPEVPTOEAEAVMLKESITVETVTOHKHKLRSASQEVGKPYLESFQNLHITKDA 267
QY 109 -----DFSPVSVTPAPSP 122

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Db 268 ASNEIPTLTKETISLOMEFNTAIYNSDDLLSSKEDKMKSETPSDSSPIEIIIDFFPT 327
QY 123 LGAAYASP
Db 328 VSAKODSPREYTDLEYSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE----- 378
QY 148 PASVSPQAEFVTPPAPAPAPPS----- 171
Db 379 -AHVSDEFKSSSSSVKVLNPNVSALESQIEMGNIVRPKVLTKAEAEKLPSTDEKDR 437
QY 172 -----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALALLSV 219
Db 438 SLTAVLSAELNKTSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALALLSV 497
QY 220 TISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRLF 279
Db 498 TISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRLF 557
QY 280 LVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN 339
Db 558 LVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLAN 617
QY 340 KNVKDMAMAKIQKIPGLKRAE 361
Db 618 KSVKDMAMAKIQKIPGLKRAE 639

RESULT 13
Q80W95
ID Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 53.3%; Score 986.8; DB 2; Length 578;
Best Local Similarity 41.1%; Pred. No. 1.1e-23;
Matches 232; Conservative 21; Mismatches 85; Indels 227; Gaps 8;

QY 7 SPLVSSD-----SPRPQAFKYQVREPEDEEEEDDEDELELV----- 54
Db 31 SPLEVPSPVSDIGIKLEPNPPYEAMSVALKTSDAKEIKEPESFNAAQAEAPYIS 90
QY 55 -----LERKPAAGLS-----AAP-----VPTAPAGALPMDFGNDFVPPA 89
Db 91 IACDLIKETKLTSPSPGFSNYSEITAKPKSVDPHCELVDSSPSEPVDFLSDSDSIPEV 150
QY 90 PR-----GLPAPAPPVAPERQSW----- 108
Db 151 POTQEAANMVKESLTFVSETVTHKHKRLSASPOEVGKPYLESFQPNLHITKDAASNE 210
QY 109 -----DPGPVSVSTVPAPPLSAA 126
Db 211 IPTLTKETISLOMEFNTAIYNSDDLLSSKEDKMKSETPSDSSPIEIIIDFFPTVSAK 270
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QY 127 AVSP----- 130
Db 271 DDSPREYTDLEYSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVDFSKSRSS 330
QY 131 -----SKLPEDDEPPARPPPPPPASVSPQAE 156
Db 331 VFVKVLLLPNVSALESQIEMGNIVRPKVLTKAEAEKLPSTDEKDR----- 376
QY 157 PWMTPPAPAPAPPSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALAL 216
Db 377 ---SLTAVLSAELNKTSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALAL 433
QY 217 LSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKEL 276
Db 434 LSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKEL 493
QY 277 RULFVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 336
Db 494 RULFVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 553
QY 337 LANKNVKDMAMAKIQKIPGLKRAE 361
Db 554 LANKNVKDMAMAKIQKIPGLKRAE 578

RESULT 14
Q6RSS8
ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name=Nogo;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Calharp S.A. Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 52.7%; Score 974.6; DB 2; Length 658;
Best Local Similarity 38.2%; Pred. No. 3.8e-23;
Matches 229; Conservative 32; Mismatches 84; Indels 254; Gaps 12;

QY 6 QSPLV-----SSDSPRPQAFKYQVREPEDE 34
Db 71 EAPLSSGTAGAEASTVQLETSQGTFTVTASVYENKKEAKPPLYQEAVMPLTQAEAK 130
QY 35 EE-----EEEEDEDELE-----ELEVLERKPAAGLSAAP----- 67
Db 131 EELTLKADRESSTSPDELTPYISACDLIKETKVSGESASPSLTDYSTTPTITEHLSQD 190
QY 68 -----VP 69
Db 191 VSEHKELAEKLSQPGKCDLFSRQVMPDPGKESDQTLILNGKSVENIETDEEQLVD 250
QY 70 TAPAGALPMDFGND-----FVPPAPRGPAPAPPVAPERQ----- 106
Db 251 SLAATGKPYLESFQDELSDSKIVTTPQSEPTPAKIAKA-EKIPLOMEELNALAYSTDVSV 309
QY 107 SWDPSVSVSTVPAPPLSAAAVSPSKLPED----- 136
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Job time : 119.158 secs

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Db 310 AMEPKPGDSKGLSPS-----SPVSVEDDFVMLVDPKGTGTEFVAEVTDRVTHKNESKD 362
QY 137 -----DEPPARPPPPASVS-----POAEPVWTPAP 164
Db 363 ISNEIRDEKROAPLTQLCDLSVRNVVEKTEDDAHALKKSQAIDREVPESMV---SLP 419
QY 165 APAAPP-----TSVVDLLYWRD 182
Db 420 ATGTSPSTKEKEIVSGKPEAKEERGAASAKEKEKPTAVFSAKLVSSVVDDLLYWRD 479
QY 183 IKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKQKSDGHPF 242
Db 480 IKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKQKSDGHPF 539
QY 243 RAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 302
Db 540 RAYLESDVAVSEELQKYSNSVVLGHNGTGVKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 599
QY 303 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE 361
Db 600 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE 658
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RESULT 15

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Q7YRW9
ID Q7YRW9 PRELIMINARY; PRT; 199 AA.
AC Q7YRW9;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactylia; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T.; Klinger M.; Stuermer C.A.; Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family."
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; AAP47319.2; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003398; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 NW; C60161DF3PB34D80 CRC64;
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Query Match 50.1%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 233
Db 12 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

QY 234 QKSDGHPFPAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVL 293
Db 72 QKSDGHPFPAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVL 131

QY 294 MWVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKI 353
Db 132 MWVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKI 191

QY 354 PGLKRAE 361
Db 192 PGLKRAE 199
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Search completed: June 23, 2005, 10:55:59